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SEQUENCE LISTING

GENERAL INFORMATION:

- (i) APPLICANT: BROW, MARY ANN D.
 LYAMICHEV, VICTOR I.
 OLIVE, DAVID M.
- (ii) TITLE OF INVENTION: RAPID DETECTION AND IDENTIFICATION OF PATHOGENS
- (iii) NUMBER OF SEQUENCES: 165
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: MEDLEN & CARROLL
 - (B) STREET: 220 MONTGOMERY STREET, SUITE 2200
 - (C) CITY: SAN FRANCISCO
 - (D) STATE: CALIFORNIA
 - (E) COUNTRY: UNITED STATES OF AMERICA
 - (F) ZIP: 94104
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: US
 - (B) FILING DATE:
 - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: CARROLL, PETER G.
 - (B) REGISTRATION NUMBER: 32,837
 - (C) REFERENCE/DOCKET NUMBER: FORS-01756
 - (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: (415) 705-8410
 - (B) TELEFAX: (415) 397-8338
- (2) INFORMATION FOR SEQ ID NO:1:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2506 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

ATGAGGGGA TGCTGCCCCT CTTTGAGCCC AAGGGCCGGG TCCTCCTGGT GGACGGCCAC 60
CACCTGGCCT ACCGCACCTT CCACGCCCTG AAGGGCCTCA CCACCAGCCG GGGGGAGCCG 120
GTGCAGGCGG TCTACGGCTT CGCCAAGAGC CTCCTCAAGGA CCCTCAAGGA GGACGGGGAC 180
GCGGTGATCG TGGTCTTTGA CGCCAAGGCC CCCTCCTTCC GCCACGAGGC CTACGGGGGG 240

TACAAGGCGG	GCCGGGCCCC	CACGCCGGAG	GACTTTCCCC	GGCAACTCGC	CCTCATCAAG	300
GAGCTGGTGG	ACCTCCTGGG	GCTGGCGCGC	CTCGAGGTCC	CGGGCTACGA	GGCGGACGAC	360
GTCCTGGCCA	GCCTGGCCAA	GAAGGCGGAA	AAGGAGGCT	ACGAGGTCCG	CATCCTCACC	420
GCCGACAAAG	ACCTTTACCA	GCTCCTTTCC	GACCGCATCC	ACGTCCTCCA	CCCCGAGGGG	480
TACCTCATCA	CCCCGGCCTG	GCTTTGGGAA	AAGTACGGCC	TGAGGCCCGA	CCAGTGGGCC	540
GACTACCGGG	CCCTGACCGG	GGACGAGTCC	GACAACCTTC	CCGGGGTCAA	GGGCATCGGG	600
GAGAAGACGG	CGAGGAAGCT	TCTGGAGGAG	TGGGGGAGCC	TGGAAGCCCT	CCTCAAGAAC	660
CTGGACCGGC	TGAAGCCCGC	CATCCGGGAG	AAGATCCTGG	CCCACATGGA	CGATCTGAAG	720
CTCTCCTGGG	ACCTGGCCAA	GGTGCGCACC	GACCTGCCCC	TGGAGGTGGA	CTTCGCCAAA	780
AGGCGGGAGC	CCGACCGGGA	GAGGCTTAGG	GCCTTTCTGG	AGAGGCTTGA	GTTTGGCAGC	840
CTCCTCCACG	AGTTCGGCCT	TCTGGAAAGC	CCCAAGGCCC	TGGAGGAGGC	CCCCTGGCCC	900
CCGCCGGAAG	GGGCCTTCGT	GGGCTTTGTG	CTTTCCCGCA	AGGAGCCCAT	GTGGGCCGAT	960
CTTCTGGCCC	TGGCCGCCGC	CAGGGGGGC	CGGGTCCACC	GGGCCCCCGA	GCCTTATAAA	1020
GCCCTCAGGG	ACCTGAAGGA	GGCGCGGGGG	CTTCTCGCCA	AAGACCTGAG	CGTTCTGGCC	1080
CTGAGGGAAG	GCCTTGGCCT	CCCGCCCGGC	GACGACCCCA	TGCTCCTCGC	CTACCTCCTG	1140
GACCCTTCCA	ACACCACCCC	CGAGGGGGTG	GCCCGGCGCT	ACGGCGGGGA	GTGGACGGAG	1200
GAGGCGGGG	AGCGGGCCGC	CCTTTCCGAG	AGGCTCTTCG	CCAACCTGTG	GGGGAGGCTT	1260
GAGGGGGAGG	AGAGGCTCCT	TTGGCTTTAC	CGGGAGGTGG	AGAGGCCCCT	TTCCGCTGTC	1320
CTGGCCCACA	TGGAGGCCAC	GGGGGTGCGC	CTGGACGTGG	CCTATCTCAG	GGCCTTGTCC	1380
CTGGAGGTGG	CCGAGGAGAT	CGCCCGCCTC	GAGGCCGAGG	TCTTCCGCCT	GGCCGGCCAC	1440
CCCTTCAACC	TCAACTCCCG	GGACCAGCTG	GAAAGGGTCC	TCTTTGACGA	GCTAGGGCTT	1500
CCCGCCATCG	GCAAGACGGA	GAAGACCGGC	AAGCGCTCCA	CCAGCGCCGC	CGTCCTGGAG	1560
GCCCTCCGCG	AGGCCCACCC	CATCGTGGAG	AAGATCCTGC	AGTACCGGGA	GCTCACCAAG	1620
CTGAAGAGCA	CCTACATTGA	CCCCTTGCCG	GACCTCATCC	ACCCCAGGAC	GGGCCGCCTC	1680
CACACCCGCT	TCAACCAGAC	GGCCACGGCC	ACGGGCAGGC	TAAGTAGCTC	CGATCCCAAC	1740
CTCCAGAACA	TCCCCGTCCG	CACCCCGCTT	GGGCAGAGGA	TCCGCCGGGC	CTTCATCGCC	1800
GAGGAGGGGT	GGCTATTGGT	GGCCCTGGAC	TATAGCCAGA	TAGAGCTCAG	GGTGCTGGCC	1860
CACCTCTCCG	GCGACGAGAA	CCTGATCCGG	GTCTTCCAGG	AGGGGCGGGA	CATCCACACG	1920
GAGACCGCCA	GCTGGATGTT	CGGCGTCCCC	CGGGAGGCCG	TGGACCCCCT	GATGCGCCGG	1980
GCGGCCAAGA	CCATCAACTT	CGGGGTCCTC	TACGGCATGT	CGGCCCACCG	CCTCTCCCAG	2040
GAGCTAGCCA	TCCCTTACGA	GGAGGCCCAG	GCCTTCATTG	AGCGCTACTT	TCAGAGCTTC	2100

CCCAAGGTGC	GGGCCTGGAT	TGAGAAGACC	CTGGAGGAGG	GCAGGAGGCG	GGGGTACGTG	2160
GAGACCCTCT	TCGGCCGCCG	CCGCTACGTG	CCAGACCTAG	AGGCCCGGGT	GAAGAGCGTG	2220
CGGGAGGCGG	CCGAGCGCAT	GGCCTTCAAC	ATGCCCGTCC	AGGGCACCGC	CGCCGACCTC	2280
ATGAAGCTGG	CTATGGTGAA	GCTCTTCCCC	AGGCTGGAGG	AAATGGGGGC	CAGGATGCTC	2340
CTTCAGGTCC	ACGACGAGCT	GGTCCTCGAG	GCCCCAAAAG	AGAGGGCGGA	GGCCGTGGCC	2400
CGGCTGGCCA	AGGAGGTCAT	GGAGGGGTG	TATCCCCTGG	CCGTGCCCCT	GGAGGTGGAG	2460
GTGGGGATAG	GGGAGGACTG	GCTCTCCGCC	AAGGAGTGAT	ACCACC		2506

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2496 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

ATGGCGATGC	TTCCCCTCTT	TGAGCCCAAA	GGCCGCGTGC	TCCTGGTGGA	CGGCCACCAC	60
CTGGCCTACC	GCACCTTCTT	TGCCCTCAAG	GGCCTCACCA	CCAGCCGCGG	CGAACCCGTT	120
CAGGCGGTCT	ACGGCTTCGC	CAAAAGCCTC	CTCAAGGCCC	TGAAGGAGGA	CGGGGACGTG	180
GTGGTGGTGG	TCTTTGACGC	CAAGGCCCCC	TCCTTCCGCC	ACGAGGCCTA	CGAGGCCTAC	240
AAGGCGGGCC	GGGCCCCCAC	CCCGGAGGAC	TTTCCCCGGC	AGCTGGCCCT	CATCAAGGAG	300
TTGGTGGACC	TCCTAGGCCT	TGTGCGGCTG	GAGGTTCCCG	GCTTTGAGGC	GGACGACGTG	360
CTGGCCACCC	TGGCCAAGCG	GGCGGAAAAG	GAGGGGTACG	AGGTGCGCAT	CCTCACTGCC	420
GACCGCGACC	TCTACCAGCT	CCTTTCGGAG	CGCATCGCCA	TCCTCCACCC	TGAGGGGTAC	480
CTGATCACCC	CGGCGTGGCT	TTACGAGAAG	TACGGCCTGC	GCCCGGAGCA	GTGGGTGGAC	540
TACCGGGCCC	TGGCGGGGGA	CCCCTCGGAT	AACATCCCCG	GGGTGAAGGG	CATCGGGGAG	600
AAGACCGCCC	AGAGGCTCAT	CCGCGAGTGG	GGGAGCCTGG	AAAACCTCTT	CCAGCACCTG	660
GACCAGGTGA	AGCCCTCCTT	GCGGGAGAAG	CTCCAGGCGG	GCATGGAGGC	CCTGGCCCTT	720
TCCCGGAAGC	TTTCCCAGGT	GCACACTGAC	CTGCCCCTGG	AGGTGGACTT	CGGGAGGCGC	780
CGCACACCCA	ACCTGGAGGG	TCTGCGGGCT	TTTTTGGAGC	GGTTGGAGTT	TGGAAGCCTC	840
CTCCACGAGT	TCGGCCTCCT	GGAGGGGCCG	AAGGCGGCAG	AGGAGGCCCC	CTGGCCCCCT	900
CCGGAAGGGG	CTTTTTTGGG	CTTTTCCTTT	TCCCGTCCCG	AGCCCATGTG	GGCCGAGCTT	960
CTGGCCCTGG	CTGGGGCGTG	GGAGGGGCGC	CTCCATCGGG	CACAAGACCC	CCTTAGGGGC	1020
CTGAGGGACC	TTAAGGGGGT	GCGGGGAATC	CTGGCCAAGG	ACCTGGCGGT	TTTGGCCCTG	1080

CGGGAGGCC	TGGACCTCTT	CCCAGAGGAC	GACCCCATGC	TCCTGGCCTA	CCTTCTGGAC	1140
CCCTCCAACA	CCACCCCTGA	GGGGGTGGCC	CGGCGTTACG	GGGGGGAGTG	GACGGAGGAT	1200
GCGGGGGAGA	GGGCCCTCCT	GGCCGAGCGC	CTCTTCCAGA	CCCTAAAGGA	GCGCCTTAAG	1260
GGAGAAGAAC	GCCTGCTTTG	GCTTTACGAG	GAGGTGGAGA	AGCCGCTTTC	CCGGGTGTTG	1320
GCCCGGATGG	AGGCCACGGG	GGTCCGGCTG	GACGTGGCCT	ACCTCCAGGC	CCTCTCCCTG	1380
GAGGTGGAGG	CGGAGGTGCG	CCAGCTGGAG	GAGGAGGTCT	TCCGCCTGGC	CGGCCACCCC	1440
TTCAACCTCA	ACTCCCGCGA	CCAGCTGGAG	CGGGTGCTCT	TTGACGAGCT	GGGCCTGCCT	1500
GCCATCGGCA	AGACGGAGAA	GACGGGGAAA	CGCTCCACCA	GCGCTGCCGT	GCTGGAGGCC	1560
CTGCGAGAGG	CCCACCCCAT	CGTGGACCGC	ATCCTGCAGT	ACCGGGAGCT	CACCAAGCTC	1620
AAGAACACCT	ACATAGACCC	CCTGCCCGCC	CTGGTCCACC	CCAAGACCGG	CCGGCTCCAC	1680
ACCCGCTTCA	ACCAGACGGC	CACCGCCACG	GGCAGGCTTT	CCAGCTCCGA	CCCCAACCTG	1740
CAGAACATCC	CCGTGCGCAC	CCCTCTGGGC	CAGCGCATCC	GCCGAGCCTT	CGTGGCCGAG	1800
GAGGGCTGGG	TGCTGGTGGT	CTTGGACTAC	AGCCAGATTG	AGCTTCGGGT	CCTGGCCCAC	1860
CTCTCCGGGG	ACGAGAACCT	GATCCGGGTC	TTTCAGGAGG	GGAGGGACAT	CCACACCCAG	1920
ACCGCCAGCT	GGATGTTCGG	CGTTTCCCCC	GAAGGGGTAG	ACCCTCTGAT	GCGCCGGGCG	1980
GCCAAGACCA	TCAACTTCGG	GGTGCTCTAC	GGCATGTCCG	CCCACCGCCT	CTCCGGGGAG	2040
CTTTCCATCC	CCTACGAGGA	GGCGGTGGCC	TTCATTGAGC	GCTACTTCCA	GAGCTACCCC	2100
AAGGTGCGGG	CCTGGATTGA	GGGGACCCTC	GAGGAGGGCC	GCCGGCGGG	GTATGTGGAG	2160
ACCCTCTTCG	GCCGCCGGCG	CTATGTGCCC	GACCTCAACG	CCCGGGTGAA	GAGCGTGCGC	2220
GAGGCGGCGG	AGCGCATGGC	CTTCAACATG	CCGGTCCAGG	GCACCGCCGC	CGACCTCATG	2280
AAGCTGGCCA	TGGTGCGGCT	TTTCCCCCGG	CTTCAGGAAC	TGGGGGCGAG	GATGCTTTTG	2340
CAGGTGCACG	ACGAGCTGGT	CCTCGAGGCC	CCCAAGGACC	GGGCGGAGAG	GGTAGCCGCT	2400
TTGGCCAAGG	AGGTCATGGA	GGGGGTCTGG	CCCCTGCAGG	TGCCCCTGGA	GGTGGAGGTG	2460
GGCCTGGGGG	AGGACTGGCT	CTCCGCCAAG	GAGTAG			2496

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2504 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

ATGGAGGCGA	TGCTTCCGCT	CTTTGAACCC	AAAGGCCGGG	TCCTCCTGGT	GGACGGCCAC	60
CACCTGGCCT	ACCGCACCTT	CTTCGCCCTG	AAGGGCCTCA	CCACGAGCCG	GGGCGAACCG	120
GTGCAGGCGG	TCTACGGCTT	CGCCAAGAGC	CTCCTCAAGG	CCCTGAAGGA	GGACGGGTAC	180
AAGGCCGTCT	TCGTGGTCTT	TGACGCCAAG	GCCCCCTCCT	TCCGCCACGA	GGCCTACGAG	240
GCCTACAAGG	CGGGGAGGGC	CCCGACCCCC	GAGGACTTCC	CCCGGCAGCT	CGCCCTCATC	300
AAGGAGCTGG	TGGACCTCCT	GGGGTTTACC	CGCCTCGAGG	TCCCCGGCTA	CGAGGCGGAC	360
GACGTTCTCG	CCACCCTGGC	CAAGAAGGCG	GAAAAGGAGG	GGTACGAGGT	GCGCATCCTC	420
ACCGCCGACC	GCGACCTCTA	CCAACTCGTC	TCCGACCGCG	TCGCCGTCCT	CCACCCGAG	480
GGCCACCTCA	TCACCCCGGA	GTGGCTTTGG	GAGAAGTACG	GCCTCAGGCC	GGAGCAGTGG	540
GTGGACTTCC	GCGCCCTCGT	GGGGGACCCC	TCCGACAACC	TCCCCGGGGT	CAAGGGCATC	600
GGGGAGAAGA	CCGCCCTCAA	GCTCCTCAAG	GAGTGGGGAA	GCCTGGAAAA	CCTCCTCAAG	660
AACCTGGACC	GGGTAAAGCC	AGAAAACGTC	CGGGAGAAGA	TCAAGGCCCA	CCTGGAAGAC	720
CTCAGGCTCT	CCTTGGAGCT	CTCCCGGGTG	CGCACCGACC	TCCCCCTGGA	GGTGGACCTC	780
GCCCAGGGGC	GGGAGCCCGA	CCGGGAGGG	CTTAGGGCCT	TCCTGGAGAG	GCTGGAGTTC	840
GGCAGCCTCC	TCCACGAGTT	CGGCCTCCTG	GAGGCCCCCG	CCCCCTGGA	GGAGGCCCCC	900
TGGCCCCCGC	CGGAAGGGGC	CTTCGTGGGC	TTCGTCCTCT	CCCGCCCCGA	GCCCATGTGG	960
GCGGAGCTTA	AAGCCCTGGC	CGCCTGCAGG	GACGGCCGGG	TGCACCGGGC	AGCAGACCCC	1020
TTGGCGGGGC	TAAAGGACCT	CAAGGAGGTC	CGGGGCCTCC	TCGCCAAGGA	CCTCGCCGTC	1080
TTGGCCTCGA	GGGAGGGGCT	AGACCTCGTG	CCCGGGGACG	ACCCCATGCT	CCTCGCCTAC	1140
CTCCTGGACC	CCTCCAACAC	CACCCCGAG	GGGGTGGCGC	GGCGCTACGG	GGGGGAGTGG	1200
ACGGAGGACG	CCGCCCACCG	GGCCCTCCTC	TCGGAGAGGC	TCCATCGGAA	CCTCCTTAAG	1260
CGCCTCGAGG	GGGAGGAGAA	GCTCCTTTGG	CTCTACCACG	AGGTGGAAAA	GCCCCTCTCC	1320
CGGGTCCTGG	CCCACATGGA	GGCCACCGGG	GTACGGCTGG	ACGTGGCCTA	CCTTCAGGCC	1380
CTTTCCCTGG	AGCTTGCGGA	GGAGATCCGC	CGCCTCGAGG	AGGAGGTCTT	CCGCTTGGCG	1440
GGCCACCCCT	TCAACCTCAA	CTCCCGGGAC	CAGCTGGAAA	GGGTGCTCTT	TGACGAGCTT	1500
AGGCTTCCCG	CCTTGGGGAA	GACGCAAAAG	ACAGGCAAGC	GCTCCACCAG	CGCCGCGGTG	1560
CTGGAGGCCC	TACGGGAGGC	CCACCCCATC	GTGGAGAAGA	TCCTCCAGCA	CCGGGAGCTC	1620
ACCAAGCTCA	AGAACACCTA	CGTGGACCCC	CTCCCAAGCC	TCGTCCACCC	GAGGACGGGC	1680
CGCCTCCACA	CCCGCTTCAA	CCAGACGGCC	ACGGCCACGG	GGAGGCTTAG	TAGCTCCGAC	1740
CCCAACCTGC	AGAACATCCC	CGTCCGCACC	CCCTTGGGCC	AGAGGATCCG	CCGGGCCTTC	1800

GTGGCCGAGG	CGGGTTGGGC	GTTGGTGGCC	CTGGACTATA	GCCAGATAGA	GCTCCGCGTC	1860
CTCGCCCACC	TCTCCGGGGA	CGAAAACCTG	ATCAGGGTCT	TCCAGGAGGG	GAAGGACATC	1920
CACACCCAGA	CCGCAAGCTG	GATGTTCGGC	GTCCCCCCGG	AGGCCGTGGA	CCCCCTGATG	1980
CGCCGGGCGG	CCAAGACGGT	GAACTTCGGC	GTCCTCTACG	GCATGTCCGC	CCATAGGCTC	2040
TCCCAGGAGC	TTGCCATCCC	CTACGAGGAG	GCGGTGGCCT	TTATAGAGGC	TACTTCCAAA	2100
GCTTCCCCAA	GGTGCGGGCC	TGGATAGAAA	AGACCCTGGA	GGAGGGGAGG	AAGCGGGGCT	2160
ACGTGGAAAC	CCTCTTCGGA	AGAAGGCGCT	ACGTGCCCGA	CCTCAACGCC	CGGGTGAAGA	2220
GCGTCAGGGA	GGCCGCGGAG	CGCATGGCCT	TCAACATGCC	CGTCCAGGGC	ACCGCCGCCG	2280
ACCTCATGAA	GCTCGCCATG	GTGAAGCTCT	TCCCCCGCCT	CCGGGAGATG	GGGGCCCGCA	2340
TGCTCCTCCA	GGTCCACGAC	GAGCTCCTCC	TGGAGGCCCC	CCAAGCGCGG	GCCGAGGAGG	2400
TGGCGGCTTT	GGCCAAGGAG	GCCATGGAGA	AGGCCTATCC	CCTCGCCGTG	CCCCTGGAGG	2460
TGGAGGTGGG	GATGGGGGAG	GACTGGCTTT	CCGCCAAGGG	TTAG		2504

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 832 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Arg Gly Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val Leu Leu 1 5 10 15

Val Asp Gly His His Leu Ala Tyr Arg Thr Phe His Ala Leu Lys Gly
20 25 30

Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly Phe Ala 35 40 45

Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Asp Ala Val Ile Val 50 60

Val Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala Tyr Gly Gly 65 70 75 80

Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln Leu 85 90 95

Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Leu Ala Arg Leu Glu 100 105 110

Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Ser Leu Ala Lys Lys 115 120 125

Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp Lys Asp 130 135 140

Leu Tyr Gln Leu Leu Ser Asp Arg Ile His Val Leu His Pro Glu Gly Tyr Leu Ile Thr Pro Ala Trp Leu Trp Glu Lys Tyr Gly Leu Arg Pro Asp Gln Trp Ala Asp Tyr Arg Ala Leu Thr Gly Asp Glu Ser Asp Asn Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Arg Lys Leu Leu Glu Glu Trp Gly Ser Leu Glu Ala Leu Leu Lys Asn Leu Asp Arg Leu Lys Pro Ala Ile Arg Glu Lys Ile Leu Ala His Met Asp Asp Leu Lys Leu Ser Trp Asp Leu Ala Lys Val Arg Thr Asp Leu Pro Leu Glu Val Asp Phe Ala Lys Arg Arg Glu Pro Asp Arg Glu Arg Leu Arg Ala Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly Leu Leu Glu Ser Pro Lys Ala Leu Glu Glu Ala Pro Trp Pro Pro Pro Glu Gly Ala Phe Val Gly Phe Val Leu Ser Arg Lys Glu Pro Met Trp Ala Asp Leu Leu Ala Leu Ala Ala Ala Arg Gly Gly Arg Val His Arg Ala Pro Glu Pro Tyr Lys Ala Leu Arg Asp Leu Lys Glu Ala Arg Gly Leu Leu Ala Lys Asp Leu Ser Val Leu Ala Leu Arg Glu Gly Leu Gly Leu Pro Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Asp Pro Ser Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Glu Trp Thr Glu Glu Ala Gly Glu Arg Ala Ala Leu Ser Glu Arg Leu Phe Ala Asn Leu Trp Gly Arg Leu Glu Gly Glu Glu Arg Leu Leu Trp Leu Tyr Arg Glu 420 425 430 Val Glu Arg Pro Leu Ser Ala Val Leu Ala His Met Glu Ala Thr Gly Val Arg Leu Asp Val Ala Tyr Leu Arg Ala Leu Ser Leu Glu Val Ala Glu Glu Ile Ala Arg Leu Glu Ala Glu Val Phe Arg Leu Ala Gly His

- Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Leu Phe Asp 495 Glu Leu Gly Leu Pro Ala Ile Gly Lys Thr Glu Lys Thr Gly Lys Arg
- Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu Ala His Pro Ile
- Val Glu Lys Ile Leu Gln Tyr Arg Glu Leu Thr Lys Leu Lys Ser Thr
- Tyr Ile Asp Pro Leu Pro Asp Leu Ile His Pro Arg Thr Gly Arg Leu 560
- His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg Leu Ser Ser 575
- Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro Leu Gly Gln 580
- Arg Ile Arg Arg Ala Phe Ile Ala Glu Glu Gly Trp Leu Leu Val Ala
- Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu Ser Gly
- Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Arg Asp Ile His Thr 640
- Glu Thr Ala Ser Trp Met Phe Gly Val Pro Arg Glu Ala Val Asp Pro 655
- Leu Met Arg Arg Ala Ala Lys Thr Ile Asn Phe Gly Val Leu Tyr Gly
- Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile Pro Tyr Glu Glu Glu
- Ala Gln Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe Pro Lys Val Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Arg Arg Gly Tyr Val 710
- Glu Thr Leu Phe Gly Arg Arg Tyr Val Pro Asp Leu Glu Ala Arg
 735 Arg
- Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn Met Pro
- Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val Lys Leu
 765 Val Lys Leu
- Phe Pro Arg Leu Glu Glu Met Gly Ala Arg Met Leu Leu Gln Val His

Asp Glu Leu Val Leu Glu Ala Pro Lys Glu Arg Ala Glu Ala Val Ala 785 790 795 800

Arg Leu Ala Lys Glu Val Met Glu Gly Val Tyr Pro Leu Ala Val Pro 805 810 815

Leu Glu Val Glu Val Gly Ile Gly Glu Asp Trp Leu Ser Ala Lys Glu 820 825 830

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 831 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Met Ala Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val Leu Leu Val
1 5 10 15

Asp Gly His His Leu Ala Tyr Arg Thr Phe Phe Ala Leu Lys Gly Leu 20 25 30

Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly Phe Ala Lys
35 40 45

Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Asp Val Val Val Val 50 55 60

Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala Tyr Glu Ala Tyr 65 70 75 80

Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln Leu Ala 85 90 95

Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Leu Val Arg Leu Glu Val 100 105 110

Pro Gly Phe Glu Ala Asp Asp Val Leu Ala Thr Leu Ala Lys Arg Ala 115 120 125

Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp Arg Asp Leu 130 135 140

Tyr Gln Leu Leu Ser Glu Arg Ile Ala Ile Leu His Pro Glu Gly Tyr 145 150 155 160

Leu Ile Thr Pro Ala Trp Leu Tyr Glu Lys Tyr Gly Leu Arg Pro Glu 165 170 175

Gln Trp Val Asp Tyr Arg Ala Leu Ala Gly Asp Pro Ser Asp Asn Ile 180 185 190

Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Gln Arg Leu Ile Arg 195 200 205

D9940925.061002

Glu Trp Gly Ser Leu Glu Asn Leu Phe Gln His Leu Asp Gln Val Lys Pro Ser Leu Arg Glu Lys Leu Gln Ala Gly Met Glu Ala Leu Ala Leu Ser Arg Lys Leu Ser Gln Val His Thr Asp Leu Pro Leu Glu Val Asp Phe Gly Arg Arg Thr Pro Asn Leu Glu Gly Leu Arg Ala Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly Leu Leu Glu Gly Pro Lys Ala Ala Glu Glu Ala Pro Trp Pro Pro Pro Glu Gly Ala Phe Leu Gly Phe Ser Phe Ser Arg Pro Glu Pro Met Trp Ala Glu Leu Leu Ala Leu Ala Gly Ala Trp Glu Gly Arg Leu His Arg Ala Gln Asp Pro Leu Arg Gly Leu Arg Asp Leu Lys Gly Val Arg Gly Ile Leu Ala Lys Asp Leu Ala Val Leu Ala Leu Arg Glu Gly Leu Asp Leu Phe Pro Glu Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Asp Pro Ser Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Trp Thr Glu Asp Ala Gly Glu Arg Ala Leu Leu Ala Glu Arg Leu Phe Gln Thr Leu Lys Glu Arg Leu Lys Gly Glu Glu Arg Leu Leu Trp Leu Tyr Glu Glu Val Glu Lys Pro Leu Ser Arg Val Leu Ala Arg Met Glu Ala Thr Gly Val Arg Leu Asp Val Ala Tyr Leu Gln Ala Leu Ser Leu Glu Val Glu Ala Glu Val Arg Gln Leu Glu Glu Val Phe Arg Leu Ala Gly His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Leu Phe Asp Glu 490 495 Leu Gly Leu Pro Ala Ile Gly Lys Thr Glu Lys Thr Gly Lys Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu Ala His Pro Ile Val Asp Arg Ile Leu Gln Tyr Arg Glu Leu Thr Lys Leu Lys Asn Thr Tyr

Ile Asp Pro Leu Pro Ala Leu Val His Pro Lys Thr Gly Arg Leu His 545 550 Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg Leu Ser Ser 565 570 Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro Leu Gly Gln Arg 585 590 Ile Arg Arg Ala Phe Val Ala Glu Glu Gly Trp Val Leu Val Val Leu 595 605 Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu Ser Gly Asp 610 615 Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Arg Asp Ile His Thr Gln 625 630 635 640 Thr Ala Ser Trp Met Phe Gly Val Ser Pro Glu Gly Val Asp Pro Leu 645 Met Arg Arg Ala Ala Lys Thr Ile Asn Phe Gly Val Leu Tyr Gly Met 665 Ser Ala His Arg Leu Ser Gly Glu Leu Ser Ile Pro Tyr Glu Glu Ala 680 Val Ala Phe Ile Glu Arg Tyr Phe Gln Ser Tyr Pro Lys Val Arg Ala 695 Trp Ile Glu Gly Thr Leu Glu Glu Gly Arg Arg Arg Gly Tyr Val Glu 705 710 715 720 Thr Leu Phe Gly Arg Arg Tyr Val Pro Asp Leu Asn Ala Arg Val 725 735 Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn Met Pro Val 740 745 750 Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val Arg Leu Phe 755 760 765 Pro Arg Leu Gln Glu Leu Gly Ala Arg Met Leu Leu Gln Val His Asp 770 775 780 Glu Leu Val Leu Glu Ala Pro Lys Asp Arg Ala Glu Arg Val Ala Ala 790 795 Leu Ala Lys Glu Val Met Glu Gly Val Trp Pro Leu Gln Val Pro Leu 805 Glu Val Glu Val Gly Leu Gly Glu Asp Trp Leu Ser Ala Lys Glu 825

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 834 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:
- Met Glu Ala Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val Leu Leu 1 5 10 15
- Val Asp Gly His His Leu Ala Tyr Arg Thr Phe Phe Ala Leu Lys Gly 20 25 30
- Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly Phe Ala 35 40 45
- Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Tyr Lys Ala Val Phe 50 60
- Val Val Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala Tyr Glu 65 70 75 80
- Ala Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln
 85 90 95
- Leu Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Phe Thr Arg Leu 100 105 110
- Glu Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Thr Leu Ala Lys 115 120 125
- Lys Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp Arg 130 135 140
- Asp Leu Tyr Gln Leu Val Ser Asp Arg Val Ala Val Leu His Pro Glu 145 150 155 160
- Gly His Leu Ile Thr Pro Glu Trp Leu Trp Glu Lys Tyr Gly Leu Arg 165 170 175
- Pro Glu Gln Trp Val Asp Phe Arg Ala Leu Val Gly Asp Pro Ser Asp 180 185 190
- Asn Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Leu Lys Leu 195 205
- Leu Lys Glu Trp Gly Ser Leu Glu Asn Leu Leu Lys Asn Leu Asp Arg 210 215 220
- Val Lys Pro Glu Asn Val Arg Glu Lys Ile Lys Ala His Leu Glu Asp 225 230 235 240
- Leu Arg Leu Ser Leu Glu Leu Ser Arg Val Arg Thr Asp Leu Pro Leu 245 250 255
- Glu Val Asp Leu Ala Gln Gly Arg Glu Pro Asp Arg Glu Gly Leu Arg 260 265 270
- Ala Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly 275 280 285
- Leu Leu Glu Ala Pro Ala Pro Leu Glu Glu Ala Pro Trp Pro Pro 290 295 300

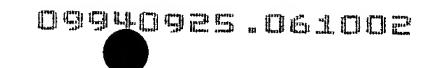
Glu Gly Ala Phe Val Gly Phe Val Leu Ser Arg Pro Glu Pro Met Trp Ala Glu Leu Lys Ala Leu Ala Ala Cys Arg Asp Gly Arg Val His Arg Ala Ala Asp Pro Leu Ala Gly Leu Lys Asp Leu Lys Glu Val Arg Gly Leu Leu Ala Lys Asp Leu Ala Val Leu Ala Ser Arg Glu Gly Leu Asp Leu Val Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Asp Pro Ser Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Trp Thr Glu Asp Ala Ala His Arg Ala Leu Leu Ser Glu Arg Leu His Arg Asn Leu Leu Lys Arg Leu Glu Gly Glu Glu Lys Leu Leu Trp Leu Tyr His Glu Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met Glu Ala Thr Gly Val Arg Leu Asp Val Ala Tyr Leu Gln Ala Leu Ser Leu Glu Leu Ala Glu Glu Ile Arg Arg Leu Glu Glu Val Phe Arg Leu Ala Gly His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Leu Phe Asp Glu Leu Arg Leu Pro Ala Leu Gly Lys Thr Gln Lys Thr Gly Lys Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu Ala His Pro Ile Val Glu Lys Ile Leu Gln His Arg Glu Leu Thr Lys Leu Lys Asn Thr Tyr Val Asp Pro Leu Pro Ser Leu Val His Pro Arg Thr Gly Arg Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg Leu Ser Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro Leu Gly Gln Arg Ile Arg Arg Ala Phe Val Ala Glu Ala Gly Trp Ala Leu Val Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu Ser Gly Asp Glu Asn Leu Ile Arq Val Phe Gln Glu Gly Lys Asp Ile

His	Thr	Gln	Thr	Ala 645	Ser	Trp	Met	Phe	Gly 650	Val	Pro	Pro	Glu	Ala 655	Val
Asp	Pro	Leu	Met 660	Arg	Arg	Ala	Ala	Lys 665	Thr	Val	Asn	Phe	Gly 670	Val	Leu
Tyr	Gly	Met 675	Ser	Ala	His	Arg	Leu 680	Ser	Gln	Glu	Leu	Ala 685	Ile	Pro	Tyr
Glu	Glu 690	Ala	Val	Ala	Phe	Ile 695	Glu	Arg	Tyr	Phe	Gln 700	Ser	Phe	Pro	Lys
Val 705	Arg	Ala	Trp	Ile	Glu 710	Lys	Thr	Leu	Glu	Glu 715	Gly	Arg	Lys	Arg	Gly 720
Tyr	Val	Glu	Thr	Leu 725	Phe	Gly	Arg	Arg	Arg 730	Tyr	Val	Pro	Asp	Leu 735	Asn
Ala	Arg	Val	Lys 740	Ser	Val	Arg	Glu	Ala 745	Ala	Glu	Arg	Met	Ala 750	Phe	Asn
Met	Pro	Val 755	Gln	Gly	Thr	Ala	Ala 760	Asp	Leu	Met	Lys	Leu 765	Ala	Met	Val
Lys	Leu 770	Phe	Pro	Arg	Leu	Arg 775	Glu	Met	Gly	Ala	Arg 780	Met	Leu	Leu	Gln
Val 785	His	Asp	Glu	Leu	Leu 790	Leu	Glu	Ala	Pro	Gln 795	Ala	Arg	Ala	Glu	Glu 800
Val	Ala	Ala	Leu	Ala 805	Lys	Glu	Ala	Met	Glu 810	Lys	Ala	Tyr	Pro	Leu 815	Ala
Val	Pro	Leu	Glu 820	Val	Glu	Val	Gly	Met 825	Gly	Glu	Asp	Trp	Leu 830	Ser	Ala
Lys	Gly														

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2502 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

ATGNNGGCGA TGCTTCCCCT CTTTGAGCCC AAAGGCCGGG TCCTCCTGGT GGACGGCCAC 60
CACCTGGCCT ACCGCACCTT CTTCGCCCTG AAGGGCCTCA CCACCAGCCG GGGCGAACCG 120
GTGCAGGCGG TCTACGGCTT CGCCAAGAGC CTCCTCAAGG CCCTGAAGGA GGACGGGGAC 180
NNGGCGGTGN TCGTGGTCTT TGACGCCAAG GCCCCCTCCT TCCGCCACGA GGCCTACGAG 240
GCCTACAAGG CGGGCCGGGC CCCCACCCCG GAGGACTTC CCCGGCAGCT CGCCCTCATC 300
AAGGAGCTGG TGGACCTCCT GGGGCTTGCG CGCCTCGAGG TCCCCGGCTA CGAGGCGGAC 360



GACGTNCTGG	CCACCCTGGC	CAAGAAGGCG	GAAAAGGAGG	GGTACGAGGT	GCGCATCCTC	420
ACCGCCGACC	GCGACCTCTA	CCAGCTCCTT	TCCGACCGCA	TCGCCGTCCT	CCACCCGAG	480
GGGTACCTCA	TCACCCCGGC	GTGGCTTTGG	GAGAAGTACG	GCCTGAGGCC	GGAGCAGTGG	540
GTGGACTACC	GGGCCCTGGC	GGGGGACCCC	TCCGACAACC	TCCCCGGGGT	CAAGGGCATC	600
GGGGAGAAGA	CCGCCCNGAA	GCTCCTCNAG	GAGTGGGGGA	GCCTGGAAAA	CCTCCTCAAG	660
AACCTGGACC	GGGTGAAGCC	CGCCNTCCGG	GAGAAGATCC	AGGCCCACAT	GGANGACCTG	720
ANGCTCTCCT	GGGAGCTNTC	CCAGGTGCGC	ACCGACCTGC	CCCTGGAGGT	GGACTTCGCC	780
AAGNGGCGGG	AGCCCGACCG	GGAGGGGCTT	AGGGCCTTTC	TGGAGAGGCT	GGAGTTTGGC	840
AGCCTCCTCC	ACGAGTTCGG	CCTCCTGGAG	GGCCCCAAGG	CCCTGGAGGA	GGCCCCCTGG	900
ccccccccg	AAGGGGCCTT	CGTGGGCTTT	GTCCTTTCCC	GCCCCGAGCC	CATGTGGGCC	960
GAGCTTCTGG	CCCTGGCCGC	CGCCAGGGAG	GGCCGGGTCC	ACCGGGCACC	AGACCCCTTT	1020
ANGGGCCTNA	GGGACCTNAA	GGAGGTGCGG	GGNCTCCTCG	CCAAGGACCT	GGCCGTTTTG	1080
GCCCTGAGGG	AGGGCCTNGA	CCTCNTGCCC	GGGGACGACC	CCATGCTCCT	CGCCTACCTC	1140
CTGGACCCCT	CCAACACCAC	CCCCGAGGGG	GTGGCCCGGC	GCTACGGGGG	GGAGTGGACG	1200
GAGGANGCGG	GGGAGCGGGC	CCTCCTNTCC	GAGAGGCTCT	TCCNGAACCT	NNNGCAGCGC	1260
CTTGAGGGGG	AGGAGAGGCT	CCTTTGGCTT	TACCAGGAGG	TGGAGAAGCC	CCTTTCCCGG	1320
GTCCTGGCCC	ACATGGAGGC	CACGGGGGTN	CGGCTGGACG	TGGCCTACCT	CCAGGCCCTN	1380
TCCCTGGAGG	TGGCGGAGGA	GATCCGCCGC	CTCGAGGAGG	AGGTCTTCCG	CCTGGCCGGC	1440
CACCCCTTCA	ACCTCAACTC	CCGGGACCAG	CTGGAAAGGG	TGCTCTTTGA	CGAGCTNGGG	1500
CTTCCCGCCA	TCGGCAAGAC	GGAGAAGACN	GGCAAGCGCT	CCACCAGCGC	CGCCGTGCTG	1560
GAGGCCCTNC	GNGAGGCCCA	CCCCATCGTG	GAGAAGATCC	TGCAGTACCG	GGAGCTCACC	1620
AAGCTCAAGA	ACACCTACAT	NGACCCCCTG	CCNGNCCTCG	TCCACCCCAG	GACGGGCCGC	1680
CTCCACACCC	GCTTCAACCA	GACGGCCACG	GCCACGGGCA	GGCTTAGTAG	CTCCGACCCC	1740
AACCTGCAGA	ACATCCCCGT	CCGCACCCCN	CTGGGCCAGA	GGATCCGCCG	GGCCTTCGTG	1800
GCCGAGGAGG	GNTGGGTGTT	GGTGGCCCTG	GACTATAGCC	AGATAGAGCT	CCGGGTCCTG	1860
GCCCACCTCT	CCGGGGACGA	GAACCTGATC	CGGGTCTTCC	AGGAGGGGAG	GGACATCCAC	1920
ACCCAGACCG	CCAGCTGGAT	GTTCGGCGTC	CCCCCGGAGG	CCGTGGACCC	CCTGATGCGC	1980
CGGGCGGCCA	AGACCATCAA	CTTCGGGGTC	CTCTACGGCA	TGTCCGCCCA	CCGCCTCTCC	2040
CAGGAGCTTG	CCATCCCCTA	CGAGGAGGCG	GTGGCCTTCA	TTGAGCGCTA	CTTCCAGAGC	2100
TTCCCCAAGG	TGCGGGCCTG	GATTGAGAAG	ACCCTGGAGG	AGGGCAGGAG	GCGGGGGTAC	2160
GTGGAGACCC	TCTTCGGCCG	CCGGCGCTAC	GTGCCCGACC	TCAACGCCCG	GGTGAAGAGC	2220

GTGCGGGAGG	CGGCGGAGCG	CATGGCCTTC	AACATGCCCG	TCCAGGGCAC	CGCCGCCGAC	2280
CTCATGAAGC	TGGCCATGGT	GAAGCTCTTC	CCCCGGCTNC	AGGAAATGGG	GGCCAGGATG	2340
CTCCTNCAGG	TCCACGACGA	GCTGGTCCTC	GAGGCCCCCA	AAGAGCGGGC	GGAGGNGGTG	2400
GCCGCTTTGG	CCAAGGAGGT	CATGGAGGGG	GTCTATCCCC	TGGCCGTGCC	CCTGGAGGTG	2460
GAGGTGGGGA	TGGGGGAGGA	CTGGCTCTCC	GCCAAGGAGT	AG		2502

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 833 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

- (ix) FEATURE:
 - (A) NAME/KEY: Modified-site
 - (B) LOCATION: 2
- (D) OTHER INFORMATION: /note= "Xaa at this position can be any amino acid."

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 63
- (D) OTHER INFORMATION: /note= "Xaa at this position can be any amino acid."

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 109
- (D) OTHER INFORMATION: /note= "Xaa at this position can be any amino acid."

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 186
- (D) OTHER INFORMATION: /note= "Xaa at this position can be any amino acid."

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 205
- (D) OTHER INFORMATION: /note= "Xaa at this position can be any amino acid."

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 209
- (D) OTHER INFORMATION: /note= "Xaa at this position can be any amino acid."

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 227..228
- (D) OTHER INFORMATION: /note= "Xaa at these positions can be any amino acid."

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 233
- (D) OTHER INFORMATION: /note= "Xaa at this position can be any amino acid."

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 240
- (D) OTHER INFORMATION: /note= "Xaa at this position can be any amino acid."

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 243..244
- (D) OTHER INFORMATION: /note= "Xaa at these positions can be any amino acid."

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 247
- (D) OTHER INFORMATION: /note= "Xaa at this position can be any amino acid."

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 260
- (D) OTHER INFORMATION: /note= "Xaa at this position can be any amino acid."

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 290
- (D) OTHER INFORMATION: /note= "Xaa at this position can be any amino acid."

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 329
- (D) OTHER INFORMATION: /note= "Xaa at this position can be any amino acid."

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 336
- (D) OTHER INFORMATION: /note= "Xaa at this position can be any amino acid."

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 340
- (D) OTHER INFORMATION: /note= "Xaa at this position can be any amino acid."

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 368
- (D) OTHER INFORMATION: /note= "Xaa at this position can be any amino acid."

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 414
- (D) OTHER INFORMATION: /note= "Xaa at this position can be any amino acid."

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 417..418
- (D) OTHER INFORMATION: /note= "Xaa at these positions can be any amino acid."

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 431
- (D) OTHER INFORMATION: /note= "Xaa at this position can be any amino acid."

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 551
- (D) OTHER INFORMATION: /note= "Xaa at this position can be any amino acid."

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 605
- (D) OTHER INFORMATION: /note= "Xaa at this position can be any amino acid."

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 773
- (D) OTHER INFORMATION: /note= "Xaa at this position can be any amino acid."

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 794
- (D) OTHER INFORMATION: /note= "Xaa at this position can be any amino acid."

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 798
- (D) OTHER INFORMATION: /note= "Xaa at this position can be any amino acid."

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 823
- (D) OTHER INFORMATION: /note= "Xaa at this position can be any amino acid."

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 833
- (D) OTHER INFORMATION: /note= "Xaa at this position can be any amino acid."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Met Xaa Ala Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val Leu Leu 1 10 15

Val Asp Gly His His Leu Ala Tyr Arg Thr Phe Phe Ala Leu Lys Gly 20 25 30

Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly Phe Ala 35 40 45

Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Asp Ala Val Xaa Val 50 55

Val Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala Tyr Glu Ala 65 70 75 80

Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln Leu 85 90 95

Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Leu Xaa Arg Leu Glu 100 105 110

Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Thr Leu Ala Lys Lys 115 120 125

Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp Arg Asp 130 135 140

Leu Tyr Gln Leu Leu Ser Asp Arg Ile Ala Val Leu His Pro Glu Gly
145 150 155 160

Tyr Leu Ile Thr Pro Ala Trp Leu Trp Glu Lys Tyr Gly Leu Arg Pro 165 170 175

Glu Gln Trp Val Asp Tyr Arg Ala Leu Xaa Gly Asp Pro Ser Asp Asn 180 185 190

Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Xaa Lys Leu Leu 195 200 205

Xaa Glu Trp Gly Ser Leu Glu Asn Leu Leu Lys Asn Leu Asp Arg Val 210 215 220

Lys Pro Xaa Xaa Arg Glu Lys Ile Xaa Ala His Met Glu Asp Leu Xaa 225 230 235 240

Leu Ser Xaa Xaa Leu Ser Xaa Val Arg Thr Asp Leu Pro Leu Glu Val 245 250 255

Asp Phe Ala Xaa Arg Arg Glu Pro Asp Arg Glu Gly Leu Arg Ala Phe 260 265 270

Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly Leu Leu 275 280 285

Glu Xaa Pro Lys Ala Leu Glu Glu Ala Pro Trp Pro Pro Pro Glu Gly 290 295 300

Ala Phe Val Gly Phe Val Leu Ser Arg Pro Glu Pro Met Trp Ala Glu 305 310 315

Leu Leu Ala Leu Ala Ala Ala Arg Xaa Gly Arg Val His Arg Ala Xaa Asp Pro Leu Xaa Gly Leu Arg Asp Leu Lys Glu Val Arg Gly Leu Leu Ala Lys Asp Leu Ala Val Leu Ala Leu Arg Glu Gly Leu Asp Leu Xaa Pro Gly Asp Pro Met Leu Leu Ala Tyr Leu Leu Asp Pro Ser Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Trp Thr Glu Asp Ala Gly Glu Arg Ala Leu Leu Ser Glu Arg Leu Phe Xaa Asn Leu Xaa Xaa Arg Leu Glu Glu Glu Arg Leu Leu Trp Leu Tyr Xaa Glu Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met Glu Ala Thr Gly Val Arg Leu Asp Val Ala Tyr Leu Gln Ala Leu Ser Leu Glu Val Ala Glu Glu Ile Arg Arg Leu Glu Glu Glu Val Phe Arg Leu Ala Gly His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Leu Phe Asp Glu Leu Gly Leu Pro Ala Ile Gly Lys Thr Glu Lys Thr Gly Lys Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu Ala His Pro Ile Val Glu Lys Ile Leu Gln Tyr Arg Glu Leu Thr Lys Leu Lys Asn Thr Tyr Ile Asp Pro Leu Pro Xaa Leu Val His Pro Arg Thr Gly Arg Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg Leu Ser Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro Leu Gly Gln Arg Ile Arg Arg Ala Phe Val Ala Glu Glu Gly Trp Xaa Leu Val Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu Ser Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Arg Asp Ile His Thr Gln Thr Ala Ser Trp Met Phe Gly Val Pro Pro Glu Ala Val Asp Pro

Leu	Met	Arg	Arg 660	Ala	Ala	Lys	Thr	Ile 665	Asn	Phe	Gly	Val	Leu 670	Tyr	Gly
Met	Ser	Ala 675	His	Arg	Leu	Ser	Gln 680	Glu	Leu	Ala	Ile	Pro 685	Tyr	Glu	Glu
Ala	Val 690	Ala	Phe	Ile	Glu	Arg 695	Tyr	Phe	Gln	Ser	Phe 700	Pro	Lys	Val	Arg
Ala 705	Trp	Ile	Glu	Lys	Thr 710	Leu	Glu	Glu	Gly	Arg 715	Arg	Arg	Gly	Tyr	Val 720
Glu	Thr	Leu	Phe	Gly 725	Arg	Arg	Arg	Tyr	Val 730	Pro	Asp	Leu	Asn	Ala 735	Arg
Val	Lys	Ser	Val 740	Arg	Glu	Ala	Ala	Glu 745	Arg	Met	Ala	Phe	Asn 750	Met	Pro
Val	Gln	Gly 755	Thr	Ala	Ala	Asp	Leu 760	Met	Lys	Leu	Ala	Met 765	Val	Lys	Leu
Phe	Pro 770	Arg	Leu	Xaa	Glu	Met 775	Gly	Ala	Arg	Met	Leu 780	Leu	Gln	Val	His
Asp 785	Glu	Leu	Val	Leu	Glu 790	Ala	Pro	Lys	Xaa	Arg 795	Ala	Glu	Xaa	Val	Ala 800
Ala	Leu	Ala	Lys	Glu 805	Val	Met	Glu	Gly	Val 810	Tyr	Pro	Leu	Ala	Val 815	Pro
Leu	Glu	Val	Glu 820	Val	Gly	Xaa	Gly	Glu 825	Asp	Trp	Leu	Ser	Ala 830	Lys	Glu
Xaa															
INFOR	INFORMATION FOR SEQ ID NO:9:														
(i)	(A) (B)	LEN TYI STI	E CHAIGTH:	164 nucle	17 ba	se p	airs	3							

- (2)
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

ATGAATTCGG GGATGCTGCC CCTCTTTGAG CCCAAGGGCC GGGTCCTCCT GGTGGACGGC 60 CACCACCTGG CCTACCGCAC CTTCCACGCC CTGAAGGGCC TCACCACCAG CCGGGGGGAG 120 CCGGTGCAGG CGGTCTACGG CTTCGCCAAG AGCCTCCTCA AGGCCCTCAA GGAGGACGGG 180 GACGCGGTGA TCGTGGTCTT TGACGCCAAG GCCCCCTCCT TCCGCCACGA GGCCTACGGG 240 GGGTACAAGG CGGGCCGGGC CCCCACGCCG GAGGACTTTC CCCGGCAACT CGCCCTCATC 300 AAGGAGCTGG TGGACCTCCT GGGGCTGGCG CGCCTCGAGG TCCCGGGCTA CGAGGCGGAC 360 GACGTCCTGG CCAGCCTGGC CAAGAAGGCG GAAAAGGAGG GCTACGAGGT CCGCATCCTC 420

ACCGCCGACA	AAGACCTTTA	CCAGCTCCTT	TCCGACCGCA	TCCACGTCCT	CCACCCGAG	480
GGGTACCTCA	TCACCCCGGC	CTGGCTTTGG	GAAAAGTACG	GCCTGAGGCC	CGACCAGTGG	540
GCCGACTACC	GGGCCCTGAC	CGGGGACGAG	TCCGACAACC	TTCCCGGGGT	CAAGGGCATC	600
GGGGAGAAGA	CGGCGAGGAA	GCTTCTGGAG	GAGTGGGGGA	GCCTGGAAGC	CCTCCTCAAG	660
AACCTGGACC	GGCTGAAGCC	CGCCATCCGG	GAGAAGATCC	TGGCCCACAT	GGACGATCTG	720
AAGCTCTCCT	GGGACCTGGC	CAAGGTGCGC	ACCGACCTGC	CCCTGGAGGT	GGACTTCGCC	780
AAAAGGCGGG	AGCCCGACCG	GGAGAGGCTT	AGGGCCTTTC	TGGAGAGGCT	TGAGTTTGGC	840
AGCCTCCTCC	ACGAGTTCGG	CCTTCTGGAA	AGCCCCAAGG	CCCTGGAGGA	GGCCCCCTGG	900
ccccccccc	AAGGGGCCTT	CGTGGGCTTT	GTGCTTTCCC	GCAAGGAGCC	CATGTGGGCC	960
GATCTTCTGG	CCCTGGCCGC	CGCCAGGGGG	GGCCGGGTCC	ACCGGGCCCC	CGAGCCTTAT	1020
AAAGCCCTCA	GGGACCTGAA	GGAGGCGCGG	GGGCTTCTCG	CCAAAGACCT	GAGCGTTCTG	1080
GCCCTGAGGG	AAGGCCTTGG	CCTCCCGCCC	GGCGACGACC	CCATGCTCCT	CGCCTACCTC	1140
CTGGACCCTT	CCAACACCAC	CCCCGAGGGG	GTGGCCCGGC	GCTACGGCGG	GGAGTGGACG	1200
GAGGAGGCGG	GGGAGCGGGC	CGCCCTTTCC	GAGAGGCTCT	TCGCCAACCT	GTGGGGGAGG	1260
CTTGAGGGGG	AGGAGAGGCT	CCTTTGGCTT	TACCGGGAGG	TGGAGAGGCC	CCTTTCCGCT	1320
GTCCTGGCCC	ACATGGAGGC	CACGGGGGTG	CGCCTGGACG	TGGCCTATCT	CAGGGCCTTG	1380
TCCCTGGAGG	TGGCCGGGGA	GATCGCCCGC	CTCGAGGCCG	AGGTCTTCCG	CCTGGCCGGC	1440
CACCCCTTCA	ACCTCAACTC	CCGGGACCAG	CTGGAAAGGG	TCCTCTTTGA	CGAGCTAGGG	1500
CTTCCCGCCA	TCGGCAAGAC	GGAGAAGACC	GGCAAGCGCT	CCACCAGCGC	CGCCGTCCTG	1560
GAGGCCCTCC	GCGAGGCCCA	CCCCATCGTG	GAGAAGATCC	TGCAGGCATG	CAAGCTTGGC	1620
ACTGGCCGTC	GTTTTACAAC	GTCGTGA				1647

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2088 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

ATGAATTCGG GGATGCTGCC CCTCTTTGAG CCCAAGGGCC GGGTCCTCCT GGTGGACGGC 60
CACCACCTGG CCTACCGCAC CTTCCACGCC CTGAAGGGCC TCACCACCAG CCGGGGGGAG 120
CCGGTGCAGG CGGTCTACGG CTTCGCCAAG AGCCTCCTCA AGGCCCTCAA GGAGGACGGG 180
GACGCGGTGA TCGTGGTCTT TGACGCCAAG GCCCCCTCCT TCCGCCACGA GGCCTACGGG 240

GGGTACAAGG CGGGCCGGGC	CCCCACGCCG	GAGGACTTTC	CCCGGCAACT	CGCCCTCATC	300
AAGGAGCTGG TGGACCTCCT	GGGGCTGGCG	CGCCTCGAGG	TCCCGGGCTA	CGAGGCGGAC	360
GACGTCCTGG CCAGCCTGGC	CAAGAAGGCG	GAAAAGGAGG	GCTACGAGGT	CCGCATCCTC	420
ACCGCCGACA AAGACCTTTA	CCAGCTCCTT	TCCGACCGCA	TCCACGTCCT	CCACCCGAG	480
GGGTACCTCA TCACCCCGGC	CTGGCTTTGG	GAAAAGTACG	GCCTGAGGCC	CGACCAGTGG	540
GCCGACTACC GGGCCCTGAC	CGGGGACGAG	TCCGACAACC	TTCCCGGGGT	CAAGGGCATC	600
GGGGAGAAGA CGGCGAGGAA	GCTTCTGGAG	GAGTGGGGGA	GCCTGGAAGC	CCTCCTCAAG	660
AACCTGGACC GGCTGAAGCC	CGCCATCCGG	GAGAAGATCC	TGGCCCACAT	GGACGATCTG	720
AAGCTCTCCT GGGACCTGGC	CAAGGTGCGC	ACCGACCTGC	CCCTGGAGGT	GGACTTCGCC	780
AAAAGGCGGG AGCCCGACCG	GGAGAGGCTT	AGGGCCTTTC	TGGAGAGGCT	TGAGTTTGGC	840
AGCCTCCTCC ACGAGTTCGG	CCTTCTGGAA	AGCCCCAAGG	CCCTGGAGGA	GGCCCCCTGG	900
CCCCCGCCGG AAGGGGCCTT	CGTGGGCTTT	GTGCTTTCCC	GCAAGGAGCC	CATGTGGGCC	960
GATCTTCTGG CCCTGGCCGC	CGCCAGGGGG	GGCCGGGTCC	ACCGGGCCCC	CGAGCCTTAT	1020
AAAGCCCTCA GGGACCTGAA	GGAGGCGCGG	GGGCTTCTCG	CCAAAGACCT	GAGCGTTCTG	1080
GCCCTGAGGG AAGGCCTTGG	CCTCCCGCCC	GGCGACGACC	CCATGCTCCT	CGCCTACCTC	1140
CTGGACCCTT CCAACACCAC	CCCCGAGGGG	GTGGCCCGGC	GCTACGGCGG	GGAGTGGACG	1200
GAGGAGCGG GGGAGCGGGC	CGCCCTTTCC	GAGAGGCTCT	TCGCCAACCT	GTGGGGGAGG	1260
CTTGAGGGGG AGGAGAGGCT	CCTTTGGCTT	TACCGGGAGG	TGGAGAGGCC	CCTTTCCGCT	1320
GTCCTGGCCC ACATGGAGGC	CACGGGGGTG	CGCCTGGACG	TGGCCTATCT	CAGGGCCTTG	1380
TCCCTGGAGG TGGCCGGGGA	GATCGCCCGC	CTCGAGGCCG	AGGTCTTCCG	CCTGGCCGGC	1440
CACCCCTTCA ACCTCAACTC	CCGGGACCAG	CTGGAAAGGG	TCCTCTTTGA	CGAGCTAGGG	1500
CTTCCCGCCA TCGGCAAGAC	GGAGAAGACC	GGCAAGCGCT	CCACCAGCGC	CGCCGTCCTG	1560
GAGGCCCTCC GCGAGGCCCA	CCCCATCGTG	GAGAAGATCC	TGCAGTACCG	GGAGCTCACC	1620
AAGCTGAAGA GCACCTACAT	TGACCCCTTG	CCGGACCTCA	TCCACCCCAG	GACGGGCCGC	1680
CTCCACACCC GCTTCAACCA	GACGGCCACG	GCCACGGGCA	GGCTAAGTAG	CTCCGATCCC	1740
AACCTCCAGA ACATCCCCGT	CCGCACCCCG	CTTGGGCAGA	GGATCCGCCG	GGCCTTCATC	1800
GCCGAGGAGG GGTGGCTATT	GGTGGCCCTG	GACTATAGCC	AGATAGAGCT	CAGGGTGCTG	1860
GCCCACCTCT CCGGCGACGA	GAACCTGATC	CGGGTCTTCC	AGGAGGGGCG	GGACATCCAC	1920
ACGGAGACCG CCAGCTGGAT	GTTCGGCGTC	CCCCGGGAGG	CCGTGGACCC	CCTGATGCGC	1980
CGGGCGGCCA AGACCATCAA	CTTCGGGGTC	CTCTACGGCA	TGTCGGCCCA	CCGCCTCTCC	2040
CAGGAGCTAG CTAGCCATCC	CTTACGAGGA	GGCCCAGGCC	TTCATTGA		2088

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 962 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

ATGAATTCGG	GGATGCTGCC	CCTCTTTGAG	CCCAAGGGCC	GGGTCCTCCT	GGTGGACGGC	60
CACCACCTGG	CCTACCGCAC	CTTCCACGCC	CTGAAGGGCC	TCACCACCAG	CCGGGGGGAG	120
CCGGTGCAGG	CGGTCTACGG	CTTCGCCAAG	AGCCTCCTCA	AGGCCCTCAA	GGAGGACGGG	180
GACGCGGTGA	TCGTGGTCTT	TGACGCCAAG	GCCCCCTCCT	TCCGCCACGA	GGCCTACGGG	240
GGGTACAAGG	CGGGCCGGGC	CCCCACGCCG	GAGGACTTTC	CCCGGCAACT	CGCCCTCATC	300
AAGGAGCTGG	TGGACCTCCT	GGGGCTGGCG	CGCCTCGAGG	TCCCGGGCTA	CGAGGCGGAC	360
GACGTCCTGG	CCAGCCTGGC	CAAGAAGGCG	GAAAAGGAGG	GCTACGAGGT	CCGCATCCTC	420
ACCGCCGACA	AAGACCTTTA	CCAGCTTCTT	TCCGACCGCA	TCCACGTCCT	CCACCCGAG	480
GGGTACCTCA	TCACCCCGGC	CTGGCTTTGG	GAAAAGTACG	GCCTGAGGCC	CGACCAGTGG	540
GCCGACTACC	GGGCCCTGAC	CGGGGACGAG	TCCGACAACC	TTCCCGGGGT	CAAGGGCATC	600
GGGGAGAAGA	CGGCGAGGAA	GCTTCTGGAG	GAGTGGGGGA	GCCTGGAAGC	CCTCCTCAAG	660
AACCTGGACC	GGCTGAAGCC	CGCCATCCGG	GAGAAGATCC	TGGCCCACAT	GGACGATCTG	720
AAGCTCTCCT	GGGACCTGGC	CAAGGTGCGC	ACCGACCTGC	CCCTGGAGGT	GGACTTCGCC	780
AAAAGGCGGG	AGCCCGACCG	GGAGAGGCTT	AGGGCCTTTC	TGGAGAGGCT	TGAGTTTGGC	840
AGCCTCCTCC	ACGAGTTCGG	CCTTCTGGAA	AGCCCCAAGT	CATGGAGGGG	GTGTATCCCC	900
TGGCCGTGCC	CCTGGAGGTG	GAGGTGGGGA	TAGGGGAGGA	CTGGCTCTCC	GCCAAGGAGT	960
GA						962

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1600 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

ATGGAATTCG	GGGATGCTGC	CCCTCTTTGA	GCCCAAGGGC	CGGGTCCTCC	TGGTGGACGG	60
CCACCACCTG	GCCTACCGCA	CCTTCCACGC	CCTGAAGGGC	CTCACCACCA	GCCGGGGGGA	120
GCCGGTGCAG	GCGGTCTACG	GCTTCGCCAA	GAGCCTCCTC	AAGGCCCTCA	AGGAGGACGG	180
GGACGCGGTG	ATCGTGGTCT	TTGACGCCAA	GGCCCCCTCC	TTCCGCCACG	AGGCCTACGG	240
GGGGTACAAG	GCGGGCCGGG	CCCCCACGCC	GGAGGACTTT	CCCCGGCAAC	TCGCCCTCAT	300
CAAGGAGCTG	GTGGACCTCC	TGGGGCTGGC	GCGCCTCGAG	GTCCCGGGCT	ACGAGGCGGA	360
CGACGTCCTG	GCCAGCCTGG	CCAAGAAGGC	GGAAAAGGAG	GGCTACGAGG	TCCGCATCCT	420
CACCGCCGAC	AAAGACCTTT	ACCAGCTCCT	TTCCGACCGC	ATCCACGTCC	TCCACCCCGA	480
GGGGTACCTC	ATCACCCCGG	CCTGGCTTTG	GGAAAAGTAC	GGCCTGAGGC	CCGACCAGTG	540
GGCCGACTAC	CGGGCCCTGA	CCGGGGACGA	GTCCGACAAC	CTTCCCGGGG	TCAAGGGCAT	600
CGGGGAGAAG	ACGGCGAGGA	AGCTTCTGGA	GGAGTGGGGG	AGCCTGGAAG	CCCTCCTCAA	660
GAACCTGGAC	CGGCTGAAGC	CCGCCATCCG	GGAGAAGATC	CTGGCCCACA	TGGACGATCT	720
GAAGCTCTCC	TGGGACCTGG	CCAAGGTGCG	CACCGACCTG	CCCCTGGAGG	TGGACTTCGC	780
CAAAAGGCGG	GAGCCCGACC	GGGAGAGGCT	TAGGGCCTTT	CTGGAGAGGC	TTGAGTTTGG	840
CAGCCTCCTC	CACGAGTTCG	GCCTTCTGGA	AAGCCCCAAG	ATCCGCCGGG	CCTTCATCGC	900
CGAGGAGGGG	TGGCTATTGG	TGGCCCTGGA	CTATAGCCAG	ATAGAGCTCA	GGGTGCTGGC	960
CCACCTCTCC	GGCGACGAGA	ACCTGATCCG	GGTCTTCCAG	GAGGGGCGGG	ACATCCACAC	1020
GGAGACCGCC	AGCTGGATGT	TCGGCGTCCC	CCGGGAGGCC	GTGGACCCCC	TGATGCGCCG	1080
GGCGGCCAAG	ACCATCAACT	TCGGGGTCCT	CTACGGCATG	TCGGCCCACC	GCCTCTCCCA	1140
GGAGCTAGCC	ATCCCTTACG	AGGAGGCCCA	GGCCTTCATT	GAGCGCTACT	TTCAGAGCTT	1200
CCCCAAGGTG	CGGGCCTGGA	TTGAGAAGAC	CCTGGAGGAG	GGCAGGAGGC	GGGGGTACGT	1260
GGAGACCCTC	TTCGGCCGCC	GCCGCTACGT	GCCAGACCTA	GAGGCCCGGG	TGAAGAGCGT	1320
GCGGGAGGCG	GCCGAGCGCA	TGGCCTTCAA	CATGCCCGTC	CGGGGCACCG	CCGCCGACCT	1380
CATGAAGCTG	GCTATGGTGA	AGCTCTTCCC	CAGGCTGGAG	GAAATGGGGG	CCAGGATGCT	1440
CCTTCAGGTC	CACGACGAGC	TGGTCCTCGA	GGCCCCAAAA	GAGAGGGCGG	AGGCCGTGGC	1500
CCGGCTGGCC	AAGGAGGTCA	TGGAGGGGGT	GTATCCCCTG	GCCGTGCCCC	TGGAGGTGGA	1560
GGTGGGGATA	GGGGAGGACT	GGCTCTCCGC	CAAGGAGTGA			1600

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(2)	INFORMATION FOR SEQ ID NO:13:	
	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 36 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
	(ii) MOLECULE TYPE: DNA (genomic)	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:	
CACC	GAATTCG GGGATGCTGC CCCTCTTTGA GCCCAA	36
(2)	INFORMATION FOR SEQ ID NO:14:	
	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 34 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
	(ii) MOLECULE TYPE: DNA (genomic)	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:	
GTG	AGATCTA TCACTCCTTG GCGGAGAGCC AGTC	34
(2)	INFORMATION FOR SEQ ID NO:15:	
	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 91 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
	(ii) MOLECULE TYPE: DNA (genomic)	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:	
TAAT	PACGACT CACTATAGGG AGACCGGAAT TCGAGCTCGC CCGGGCGAGC TCGAATTCCG	60
TGT	ATTCTAT AGTGTCACCT AAATCGAATT C	91
(2)	INFORMATION FOR SEQ ID NO:16:	
	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 20 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
	(ii) MOLECULE TYPE: DNA (genomic)	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:	

TAATACGACT CACTATAGGG

(2)	INFO.	RMATION FOR SEQ ID NO:17:	
	(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 27 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
	(ii)	MOLECULE TYPE: DNA (genomic)	
	(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:17:	
GAA.	rtcga'	TT TAGGTGACAC TATAGAA	27
(2)	INFO	RMATION FOR SEQ ID NO:18:	
	(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 31 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
	(ii)	MOLECULE TYPE: DNA (genomic)	
	(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:18:	
GTA	ATCAT	GG TCATAGCTGG TAGCTTGCTA C	31
(2)	INFO	RMATION FOR SEQ ID NO:19:	
	(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 42 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
	(ii)	MOLECULE TYPE: DNA (genomic)	
	(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:19:	
GGA'	TCCTC	TA GAGTCGACCT GCAGGCATGC CTACCTTGGT AG	42
(2)	INFO	RMATION FOR SEQ ID NO:20:	
	(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 30 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
	(ii)	MOLECULE TYPE: DNA (genomic)	
	(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:20:	
GGA'	TCCTC	TA GAGTCGACCT GCAGGCATGC	30

(2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2502 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

ATGAATTCGG	GGATGCTGCC	CCTCTTTGAG	CCCAAGGGCC	GGGTCCTCCT	GGTGGACGGC	60
CACCACCTGG	CCTACCGCAC	CTTCCACGCC	CTGAAGGGCC	TCACCACCAG	CCGGGGGGAG	120
CCGGTGCAGG	CGGTCTACGG	CTTCGCCAAG	AGCCTCCTCA	AGGCCCTCAA	GGAGGACGGG	180
GACGCGGTGA	TCGTGGTCTT	TGACGCCAAG	GCCCCTCCT	TCCGCCACGA	GGCCTACGGG	240
GGGTACAAGG	CGGGCCGGGC	CCCCACGCCG	GAGGACTTTC	CCCGGCAACT	CGCCCTCATC	300
AAGGAGCTGG	TGGACCTCCT	GGGGCTGGCG	CGCCTCGAGG	TCCCGGGCTA	CGAGGCGGAC	360
GACGTCCTGG	CCAGCCTGGC	CAAGAAGGCG	GAAAAGGAGG	GCTACGAGGT	CCGCATCCTC	420
ACCGCCGACA	AAGACCTTTA	CCAGCTCCTT	TCCGACCGCA	TCCACGTCCT	CCACCCGAG	480
GGGTACCTCA	TCACCCCGGC	CTGGCTTTGG	GAAAAGTACG	GCCTGAGGCC	CGACCAGTGG	540
GCCGACTACC	GGGCCCTGAC	CGGGGACGAG	TCCGACAACC	TTCCCGGGGT	CAAGGGCATC	600
GGGGAGAAGA	CGGCGAGGAA	GCTTCTGGAG	GAGTGGGGGA	GCCTGGAAGC	CCTCCTCAAG	660
AACCTGGACC	GGCTGAAGCC	CGCCATCCGG	GAGAAGATCC	TGGCCCACAT	GGACGATCTG	720
AAGCTCTCCT	GGGACCTGGC	CAAGGTGCGC	ACCGACCTGC	CCCTGGAGGT	GGACTTCGCC	780
AAAAGGCGGG	AGCCCGACCG	GGAGAGGCTT	AGGGCCTTTC	TGGAGAGGCT	TGAGTTTGGC	840
AGCCTCCTCC	ACGAGTTCGG	CCTTCTGGAA	AGCCCCAAGG	CCCTGGAGGA	GGCCCCCTGG	900
CCCCCGCCGG	AAGGGCCTT	CGTGGGCTTT	GTGCTTTCCC	GCAAGGAGCC	CATGTGGGCC	960
GATCTTCTGG	CCCTGGCCGC	CGCCAGGGGG	GGCCGGGTCC	ACCGGGCCCC	CGAGCCTTAT	1020
AAAGCCCTCA	GGGACCTGAA	GGAGGCGCGG	GGGCTTCTCG	CCAAAGACCT	GAGCGTTCTG	1080
GCCCTGAGGG	AAGGCCTTGG	CCTCCCGCCC	GGCGACGACC	CCATGCTCCT	CGCCTACCTC	1140
CTGGACCCTT	CCAACACCAC	CCCCGAGGGG	GTGGCCCGGC	GCTACGGCGG	GGAGTGGACG	1200
GAGGAGGCGG	GGGAGCGGGC	CGCCCTTTCC	GAGAGGCTCT	TCGCCAACCT	GTGGGGGAGG	1260
CTTGAGGGGG	AGGAGAGGCT	CCTTTGGCTT	TACCGGGAGG	TGGAGAGGCC	CCTTTCCGCT	1320
GTCCTGGCCC	ACATGGAGGC	CACGGGGGTG	CGCCTGGACG	TGGCCTATCT	CAGGGCCTTG	1380
TCCCTGGAGG	TGGCCGGGGA	GATCGCCCGC	CTCGAGGCCG	AGGTCTTCCG	CCTGGCCGGC	1440
CACCCCTTCA	ACCTCAACTC	CCGGGACCAG	CTGGAAAGGG	TCCTCTTTGA	CGAGCTAGGG	1500

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CTTCCCGCCA	TCGGCAAGAC	GGAGAAGACC	GGCAAGCGCT	CCACCAGCGC	CGCCGTCCTG	1560
GAGGCCCTCC	GCGAGGCCCA	CCCCATCGTG	GAGAAGATCC	TGCAGTACCG	GGAGCTCACC	1620
AAGCTGAAGA	GCACCTACAT	TGACCCCTTG	CCGGACCTCA	TCCACCCCAG	GACGGGCCGC	1680
CTCCACACCC	GCTTCAACCA	GACGGCCACG	GCCACGGGCA	GGCTAAGTAG	CTCCGATCCC	1740
AACCTCCAGA	ACATCCCCGT	CCGCACCCCG	CTTGGGCAGA	GGATCCGCCG	GGCCTTCATC	1800
GCCGAGGAGG	GGTGGCTATT	GGTGGCCCTG	GACTATAGCC	AGATAGAGCT	CAGGGTGCTG	1860
GCCCACCTCT	CCGGCGACGA	GAACCTGATC	CGGGTCTTCC	AGGAGGGGCG	GGACATCCAC	1920
ACGGAGACCG	CCAGCTGGAT	GTTCGGCGTC	CCCCGGGAGG	CCGTGGACCC	CCTGATGCGC	1980
CGGGCGGCCA	AGACCATCAA	CTTCGGGGTC	CTCTACGGCA	TGTCGGCCCA	CCGCCTCTCC	2040
CAGGAGCTAG	CCATCCCTTA	CGAGGAGGCC	CAGGCCTTCA	TTGAGCGCTA	CTTTCAGAGC	2100
TTCCCCAAGG	TGCGGGCCTG	GATTGAGAAG	ACCCTGGAGG	AGGGCAGGAG	GCGGGGGTAC	2160
GTGGAGACCC	TCTTCGGCCG	CCGCCGCTAC	GTGCCAGACC	TAGAGGCCCG	GGTGAAGAGC	2220
GTGCGGGAGG	CGGCCGAGCG	CATGGCCTTC	AACATGCCCG	TCCGGGGCAC	CGCCGCCGAC	2280
CTCATGAAGC	TGGCTATGGT	GAAGCTCTTC	CCCAGGCTGG	AGGAAATGGG	GGCCAGGATG	2340
CTCCTTCAGG	TCCACGACGA	GCTGGTCCTC	GAGGCCCCAA	AAGAGAGGC	GGAGGCCGTG	2400
GCCCGGCTGG	CCAAGGAGGT	CATGGAGGGG	GTGTATCCCC	TGGCCGTGCC	CCTGGAGGTG	2460
GAGGTGGGGA	TAGGGGAGGA	CTGGCTCTCC	GCCAAGGAGT	GA		2502

- (2) INFORMATION FOR SEQ ID NO:22:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 base pairs(B) TYPE: nucleic acid

 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

GATTTAGGTG ACACTATAG

(2) INFORMATION FOR SEQ ID NO:23:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 72 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:	
CGGACGAACA AGCGAGACAG CGACACAGGT ACCACATGGT ACAAGAGGCA AGAGAGACGA	60
CACAGCAGAA AC	72
(2) INFORMATION FOR SEQ ID NO:24:	
(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 70 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: single(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: DNA (genomic)	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:	
GTTTCTGCTG TGTCGTCTCT CTTGCCTCTT GTACCATGTG GTACCTGTGT CGCTGTCTCG	60
CTTGTTCGTC	70
(2) INFORMATION FOR SEQ ID NO:25:	
(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 20 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: single(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: DNA (genomic)	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:	
GACGAACAAG CGAGACAGCG	20
(2) INFORMATION FOR SEQ ID NO:26:	
(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 24 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: single(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: DNA (genomic)	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:	
GTTTCTGCTG TGTCGTCTCT CTTG	24
(2) INFORMATION FOR SEQ ID NO:27:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 46 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
(ii) MOLECULE TYPE: DNA (genomic)	

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:	
CCTCTTGTAC CATGTGGTAC CTGTGTCGCT GTCTCGCTTG TTCGTC	46
(2) INFORMATION FOR SEQ ID NO:28:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 50 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
(ii) MOLECULE TYPE: DNA (genomic)	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:	
ACACAGGTAC CACATGGTAC AAGAGGCAAG AGAGACGACA CAGCAGAAAC	50
(2) INFORMATION FOR SEQ ID NO:29:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 15 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: single (D) TOPOLOGY: unknown 	
(ii) MOLECULE TYPE: protein	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:	
Met Ala Ser Met Thr Gly Gly Gln Gln Met Gly Arg Ile Asn Ser 1 5 10 15	
(2) INFORMATION FOR SEQ ID NO:30:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 969 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
(ii) MOLECULE TYPE: DNA (genomic)	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:	
ATGGCTAGCA TGACTGGTGG ACAGCAAATG GGTCGGATCA ATTCGGGGAT GCTGCCCCTC	60
TTTGAGCCCA AGGGCCGGGT CCTCCTGGTG GACGGCCACC ACCTGGCCTA CCGCACCTTC	120
CACGCCTGA AGGGCCTCAC CACCAGCCGG GGGGAGCCGG TGCAGGCGGT CTACGGCTTC	180
GCCAAGAGCC TCCTCAAGGC CCTCAAGGAG GACGGGGACG CGGTGATCGT GGTCTTTGAC	240
GCCAAGGCCC CCTCCTTCCG CCACGAGGCC TACGGGGGGT ACAAGGCGGG CCGGGCCCCC	300
ACGCCGGAGG ACTTTCCCCG GCAACTCGCC CTCATCAAGG AGCTGGTGGA CCTCCTGGGG	360
CTGGCGCCC TCGAGGTCCC GGGCTACGAG GCGGACGACG TCCTGGCCAG CCTGGCCAAG	420
AAGGCGGAAA AGGAGGGCTA CGAGGTCCGC ATCCTCACCG CCGACAAAGA CCTTTACCAG	480

CTTCTTTCCG ACCGCATCCA CGTCCTCCAC CCCGAGGGGT ACCTCATCAC CCCGGCCTGG

CTTTGGGAAA	AGTACGGCCT	GAGGCCCGAC	CAGTGGGCCG	ACTACCGGGC	CCTGACCGGG	600
GACGAGTCCG	ACAACCTTCC	CGGGGTCAAG	GGCATCGGGG	AGAAGACGGC	GAGGAAGCTT	660
CTGGAGGAGT	GGGGGAGCCT	GGAAGCCCTC	CTCAAGAACC	TGGACCGGCT	GAAGCCCGCC	720
ATCCGGGAGA	AGATCCTGGC	CCACATGGAC	GATCTGAAGC	TCTCCTGGGA	CCTGGCCAAG	780
GTGCGCACCG	ACCTGCCCCT	GGAGGTGGAC	TTCGCCAAAA	GGCGGGAGCC	CGACCGGGAG	840
AGGCTTAGGG	CCTTTCTGGA	GAGGCTTGAG	TTTGGCAGCC	TCCTCCACGA	GTTCGGCCTT	900
CTGGAAAGCC	CCAAGTCATG	GAGGGGGTGT	ATCCCCTGGC	CGTGCCCCTG	GAGGTGGAGG	960
TGGGGATAG						969

(2) INFORMATION FOR SEQ ID NO:31:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 948 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double

 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

ATGGCTAGCA	TGACTGGTGG	ACAGCAAATG	GGTCGGATCA	ATTCGGGGAT	GCTGCCCCTC	60
TTTGAGCCCA	AGGGCCGGGT	CCTCCTGGTG	GACGGCCACC	ACCTGGCCTA	CCGCACCTTC	120
CACGCCCTGA	AGGGCCTCAC	CACCAGCCGG	GGGGAGCCGG	TGCAGGCGGT	CTACGGCTTC	180
GCCAAGAGCC	TCCTCAAGGC	CCTCAAGGAG	GACGGGGACG	CGGTGATCGT	GGTCTTTGAC	240
GCCAAGGCCC	CCTCCTTCCG	CCACGAGGCC	TACGGGGGGT	ACAAGGCGGG	CCGGGCCCCC	300
ACGCCGGAGG	ACTTTCCCCG	GCAACTCGCC	CTCATCAAGG	AGCTGGTGGA	CCTCCTGGGG	360
CTGGCGCGCC	TCGAGGTCCC	GGGCTACGAG	GCGGACGACG	TCCTGGCCAG	CCTGGCCAAG	420
AAGGCGGAAA	AGGAGGGCTA	CGAGGTCCGC	ATCCTCACCG	CCGACAAAGA	CCTTTACCAG	480
CTTCTTTCCG	ACCGCATCCA	CGTCCTCCAC	CCCGAGGGGT	ACCTCATCAC	CCCGGCCTGG	540
CTTTGGGAAA	AGTACGGCCT	GAGGCCCGAC	CAGTGGGCCG	ACTACCGGGC	CCTGACCGGG	600
GACGAGTCCG	ACAACCTTCC	CGGGGTCAAG	GGCATCGGGG	AGAAGACGGC	GAGGAAGCTT	660
CTGGAGGAGT	GGGGAGCCT	GGAAGCCCTC	CTCAAGAACC	TGGACCGGCT	GAAGCCCGCC	720
ATCCGGGAGA	AGATCCTGGC	CCACATGGAC	GATCTGAAGC	TCTCCTGGGA	CCTGGCCAAG	780
GTGCGCACCG	ACCTGCCCCT	GGAGGTGGAC	TTCGCCAAAA	GGCGGGAGCC	CGACCGGGAG	840
AGGCTTAGGG	CCTTTCTGGA	GAGGCTTGAG	TTTGGCAGCC	TCCTCCACGA	GTTCGGCCTT	900
CTGGAAAGCC	CCAAGGCCGC	ACTCGAGCAC	CACCACCACC	ACCACTGA		948

(2) INFORMATION FOR SEQ ID NO:32:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 206 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
(ii) MOLECULE TYPE: DNA (genomic)	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:	
CGCCAGGGTT TTCCCAGTCA CGACGTTGTA AAACGACGGC CAGTGAATTG TAATACGACT	60
CACTATAGGG CGAATTCGAG CTCGGTACCC GGGGATCCTC TAGAGTCGAC CTGCAGGCAT	120
GCAAGCTTGA GTATTCTATA GTGTCACCTA AATAGCTTGG CGTAATCATG GTCATAGCTG	180
TTTCCTGTGT GAAATTGTTA TCCGCT	206
(2) INFORMATION FOR SEQ ID NO:33:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 43 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
(ii) MOLECULE TYPE: DNA (genomic)	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:	
TTCTGGGTTC TCTGCTCTCT GGTCGCTGTC TCGCTTGTTC GTC	43
(2) INFORMATION FOR SEQ ID NO:34:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 19 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
(ii) MOLECULE TYPE: DNA (genomic)	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:	
GCTGTCTCGC TTGTTCGTC	19
(2) INFORMATION FOR SEQ ID NO:35:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 20 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:	
GACGAACAAG CGAGACAGCG	20
(2) INFORMATION FOR SEQ ID NO:36:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 24 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
(ii) MOLECULE TYPE: DNA (genomic)	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:	
TTCTGGGTTC TCTGCTCTC GGTC	24
(2) INFORMATION FOR SEQ ID NO:37:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 43 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
(ii) MOLECULE TYPE: DNA (genomic)	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:	
GACGAACAAG CGAGACAGCG ACCAGAGAGC AGAGAACCCA GAA	43
(2) INFORMATION FOR SEQ ID NO:38:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 23 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
(ii) MOLECULE TYPE: DNA (genomic)	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:	
ACCAGAGAGC AGAGAACCCA GAA	23
(2) INFORMATION FOR SEQ ID NO:39:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 21 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
(ii) MOLECULE TYPE: DNA (genomic)	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:	
AACAGCTATG ACCATGATTA C	21

 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 157 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
(ii) MOLECULE TYPE: DNA (genomic)	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:	
CACCGTCCTC TTCAAGAAGT TTATCCAGAA GCCAATGCAC CCATTGGACA TAACCGGGAA	60
TCCTACATGG TTCCTTTTAT ACCACTGTAC AGAAATGGTG ATTTCTTTAT TTCATCCAAA	120
GATCTGGGCT ATGACTATAG CTATCTACAA GATTCAG	157
(2) INFORMATION FOR SEQ ID NO:41:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 157 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
(ii) MOLECULE TYPE: DNA (genomic)	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:	
CACCGTCCTC TTCAAGAAGT TTATCCAGAA GCCAATGCAC CCATTAGACA TAACCGGGAA	60
TCCTACATGG TTCCTTTTAT ACCACTGTAC AGAAATGGTG ATTTCTTTAT TTCATCCAAA	120
GATCTGGGCT ATGACTATAG CTATCTACAA GATTCAG	157
(2) INFORMATION FOR SEQ ID NO:42:	
(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 19 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: single(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: DNA (genomic)	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:	
CACCGTCCTC TTCAAGAAG	19
(2) INFORMATION FOR SEQ ID NO:43:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 20 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
(ii) MOLECULE TYPE: DNA (genomic)	

(2) INFORMATION FOR SEQ ID NO:40:

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:	
CTGAATCTTG TAGATAGCTA	20
(2) INFORMATION FOR SEQ ID NO:44	
(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 339 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: DNA (genomic)	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:	
GCCTTATTTT ACTTTAAAAA TTTTCAAATG TTTCTTTAT ACACAATATG TTTCTTAGTC	60
TGAATAACCT TTTCCTCTGC AGTATTTTTG AGCAGTGGCT CCGAAGGCAC CGTCCTCTTC	120
AAGAAGTTTA TCCAGAAGCC AATGCACCCA TTAGACATAA CCGGGAATCC TACATGGTTC	180
CTTTTATACC ACTGTACAGA AATGGTGATT TCTTTATTTC ATCCAAAGAT CTGGGCTATG	240
ACTATAGCTA TCTACAAGAT TCAGGTAAAG TTTACTTTCT TTCAGAGGAA TTGCTGAATC	300
TAGTGTTACC AATTTATTTT GAGATAACAC AAAACTTTA	339
(2) INFORMATION FOR SEQ ID NO:45:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 21 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
(ii) MOLECULE TYPE: DNA (genomic)	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:	
GCCTTATTTT ACTTTAAAAA T	21
(2) INFORMATION FOR SEQ ID NO:46:	
(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 20 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: single(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: DNA (genomic)	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:	

TAAAGTTTTG TGTTATCTCA

(2) INFORMATION FOR SEQ ID NO:47:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 157 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
(ii) MOLECULE TYPE: DNA (genomic)	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:	
CACCGTCCTC TTCAAGAAGT TTATCCAGAA GCCAATGCAC CCATTGGACA TAACCGGGAA	60
TCCTACATGG TTCCTTTAT ACCACTGTAC AGAAATGGTG ATTTCTTTAT TTCATCCAAA	120
GATCTGGGCT ATGACTATAG CTATCTACAA GATTCAG	157
(2) INFORMATION FOR SEQ ID NO:48:	
(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 157 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: DNA (genomic)	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:	
CTGAATCTTG TAGATAGCTA TAGTCATAGC CCAGATCTTT GGATGAAATA AAGAAATCAC	60
CATTTCTGTA CAGTGGTATA AAAGGAACCA TGTAGGATTC CCGGTTATGT CCAATGGGTG	120
CATTGGCTTC TGGATAAACT TCTTGAAGAG GACGGTG	157
(2) INFORMATION FOR SEQ ID NO:49:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 165 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
(ii) MOLECULE TYPE: DNA (genomic)	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:	
AGCGGATAAC AATTTCACAC AGGAAACAGC TATGACCATG ATTACGCCAA GCTATTTAGG	60
TGACACTATA GAATACTCAA GCTTGCATGC CTGCAGGTCG ACTCTAGAGG ATCCCCGGGT	120
ACCGAGCTCG AATTCGCCCT ATAGTGAGTC GTATTAGGAT CCGTG	165
(2) INFORMATION FOR SEQ ID NO:50:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 206 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	

(11) MOLECULE TYPE: DNA (genomic)	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:	
CGCCAGGGTT TTCCCAGTCA CGACGTTGTA AAACGACGGC CAGTGAATTG TAATACGACT	60
CACTATAGGG CGAATTCGAG CTCGGTACCC GGGGATCCTC TAGAGTCGAC CTGCAGGCAT	120
GCAAGCTTGA GTATTCTATA GTGTCACCTA AATAGCTTGG CGTAATCATG GTCATAGCTG	180
TTTCCTGTGT GAAATTGTTA TCCGCT	206
(2) INFORMATION FOR SEQ ID NO:51:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 24 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
(ii) MOLECULE TYPE: DNA (genomic)	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:	
AGCGGATAAC AATTTCACAC AGGA	24
(2) INFORMATION FOR SEQ ID NO:52:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 29 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
(ii) MOLECULE TYPE: DNA (genomic)	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:	
CACGGATCCT AATACGACTC ACTATAGGG	29
(2) INFORMATION FOR SEQ ID NO:53:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 24 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
(ii) MOLECULE TYPE: DNA (genomic)	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:	
CGCCAGGGTT TTCCCAGTCA CGAC	24
(2) INFORMATION FOR SEQ ID NO:54:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 157 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	

(ii) MOLECULE TYPE: DNA (genomic)	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:	
CACCGTCCTC TTCAAGAAGT TTATCCAGAA GCCAATGCAC CCATTAGACA TAACCGGGAA	60
TCCTACATGG TTCCTTTTAT ACCACTGTAC AGAAATGGTG ATTTCTTTAT TTCATCCAAA	120
GATCTGGGCT ATGACTATAG CTATCTACAA GATTCAG	157
(2) INFORMATION FOR SEQ ID NO:55:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 157 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
(ii) MOLECULE TYPE: DNA (genomic)	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:	
CACCGTCCTC TTCAAGAAGT TTATCCAGAA GCCAATGCAC CCATTGGACA TAACCAGGAA	60
TCCTACATGG TTCCTTTAT ACCACTGTAC AGAAATGGTG ATTTCTTTAT TTCATCCAAA	120
GATCTGGGCT ATGACTATAG CTATCTACAA GATTCAG	157
(2) INFORMATION FOR SEQ ID NO:56:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 378 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
(ii) MOLECULE TYPE: DNA (genomic)	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:	
CACCGTCCTC TTCAAGAAGT TTATCCAGAA GCCAATGCAC CCATTGGACA TAACCGGGAA	60
TCCTACATGG TTCCTTTTAT ACCACTGTAC AGAAATGGTG ATTTCTTTAT TTCATCCAAA	120
GATCTGGGCT ATGACTATAG CTATCTACAA GATTCAGACC CAGACTCTTT TCAAGACTAC	180
ATTAAGTCCT ATTTGGAACA AGCGAGTCGG ATCTGGTCAT GGCTCCTTGG GGCGGCGATG	240
GTAGGGGCCG TCCTCACTGC CCTGCTGGCA GGGCTTGTGA GCTTGCTGTG TCGTCACAAG	300
AGAAAGCAGC TTCCTGAAGA AAAGCAGCCA CTCCTCATGG AGAAAGAGGA TTACCACAGC	360
TTGTATCAGA GCCATTTA	378
(2) INFORMATION FOR SEQ ID NO:57:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 378 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	

- (ii) MOLECULE TYPE: DNA (genomic)
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

CACCGTCCTC	TTCAAGAAGT	TTATCCAGAA	GCCAATGCAC	CCATTGGACA	TAACCAGGAA	60
TCCTACATGG	TTCCTTTTAT	ACCACTGTAC	AGAAATGGTG	ATTTCTTTAT	TTCATCCAAA	120
GATCTGGGCT	ATGACTATAG	CTATCTACAA	GATTCAGACC	CAGACTCTTT	TCAAGACTAC	180
ATTAAGTCCT	ATTTGGAACA	AGCGAGTCGG	ATCTGGTCAT	GGCTCCTTGG	GGCGGCGATG	240
GTAGGGGCCG	TCCTCACTGC	CCTGCTGGCA	GGGCTTGTGA	GCTTGCTGTG	TCGTCACAAG	300
AGAAAGCAGC	TTCCTGAAGA	AAAGCAGCCA	CTCCTCATGG	AGAAAGAGGA	TTACCACAGC	360
TTGTATCAGA	GCCATTTA					378

- (2) INFORMATION FOR SEQ ID NO:58:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1059 base pairs
 (B) TYPE: nucleic acid

 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

GCAAGTTTGG	CTTTTGGGGA	CCAAACTGCA	CAGAGAGACG	ACTCTTGGTG	AGAAGAAACA	60
TCTTCGATTT	GAGTGCCCCA	GAGAAGGACA	AATTTTTTGC	CTACCTCACT	TTAGCAAAGC	120
ATACCATCAG	CTCAGACTAT	GTCATCCCCA	TAGGGACCTA	TGGCCAAATG	AAAAATGGAT	180
CAACACCCAT	GTTTAACGAC	ATCAATATTT	ATGACCTCTT	TGTCTGGATG	CATTATTATG	240
TGTCAATGGA	TGCACTGCTT	GGGGGATATG	AAATCTGGAG	AGACATTGAT	TTTGCCCATG	300
AAGCACCAGC	TTTTCTGCCT	TGGCATAGAC	TCTTCTTGTT	GCGGTGGGAA	CAAGAAATCC	360
AGAAGCTGAC	AGGAGATGAA	AACTTCACTA	TTCCATATTG	GGACTGGCGG	GATGCAGAAA	420
AGTGTGACAT	TTGCACAGAT	GAGTACATGG	GAGGTCAGCA	CCCCACAAAT	CCTAACTTAC	480
TCAGCCCAGC	ATCATTCTTC	TCCTCTTGGC	AGATTGTCTG	TAGCCGATTG	GAGGAGTACA	540
ACAGCCATCA	GTCTTTATGC	AATGGAACGC	CCGAGGGACC	TTTACGGCGT	AATCCTGGAA	600
ACCATGACAA	ATCCAGAACC	CCAAGGCTCC	CCTCTTCAGC	TGATGTAGAA	TTTTGCCTGA	660
GTTTGACCCA	ATATGAATCT	GGTTCCATGG	ATAAAGCTGC	CAATTTCAGC	TTTAGAAATA	720
CACTGGAAGG	ATTTGCTAGT	CCACTTACTG	GGATAGCGGA	TGCCTCTCAA	AGCAGCATGC	780
ACAATGCCTT	GCACATCTAT	ATGAATGGAA	CAATGTCCCA	GGTACAGGGA	TCTGCCAACG	840
ATCCTATCTT	CCTTCTTCAC	CATGCATTTG	TTGACAGTAT	TTTTGAGCAG	TGGCTCCGAA	900
GGCACCGTCC	TCTTCAAGAA	GTTTATCCAG	AAGCCAATGC	ACCCATTGGA	CATAACCGGG	960

AATCCTACAT GGTTCCTTTT ATACCACTGT ACAGAAATGG TGATTTCTTT ATTTCATCCA 1020 1059 AAGATCTGGG CTATGACTAT AGCTATCTAC AAGATTCAG

- (2) INFORMATION FOR SEQ ID NO:59:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1059 base pairs(B) TYPE: nucleic acid

 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

GCAAGTTTGG	CTTTTGGGGA	CCAAACTGCA	CAGAGAGACG	ACTCTTGGTG	AGAAGAAACA	60
TCTTCGATTT	GAGTGCCCCA	GAGAAGGACA	AATTTTTTGC	CTACCTCACT	TTAGCAAAGC	120
ATACCATCAG	CTCAGACTAT	GTCATCCCCA	TAGGGACCTA	TGGCCAAATG	AAAAATGGAT	180
CAACACCCAT	GTTTAACGAC	ATCAATATTT	ATGACCTCTT	TGTCTGGATG	CATTATTATG	240
TGTCAATGGA	TGCACTGCTT	GGGGGATATG	AAATCTGGAG	AGACATTGAT	TTTGCCCATG	300
AAGCACCAGC	TTTTCTGCCT	TGGCATAGAC	TCTTCTTGTT	GCGGTGGGAA	CAAGAAATCC	360
AGAAGCTGAC	AGGAGATGAA	AACTTCACTA	TTCCATATTG	GGACTGGCGG	GATGCAGAAA	420
AGTGTGACAT	TTGCACAGAT	GAGTACATGG	GAGGTCAGCA	CCCCACAAAT	CCTAACTTAC	480
TCAGCCCAGC	ATCATTCTTC	TCCTCTTGGC	AGATTGTCTG	TAGCCGATTG	GAGGAGTACA	540
ACAGCCATCA	GTCTTTATGC	AATGGAACGC	CCGAGGGACC	TTTACGGCGT	AATCCTGGAA	600
ACCATGACAA	ATCCAGAACC	CCAAGGCTCC	CCTCTTCAGC	TGATGTAGAA	TTTTGCCTGA	660
GTTTGACCCA	ATATGAATCT	GGTTCCATGG	ATAAAGCTGC	CAATTTCAGC	TTTAGAAATA	720
CACTGGAAGG	ATTTGCTAGT	CCACTTACTG	GGATAGCGGA	TGCCTCTCAA	AGCAGCATGC	780
ACAATGCCTT	GCACATCTAT	ATGAATGGAA	CAATGTCCCA	GGTACAGGGA	TCTGCCAACG	840
ATCCTATCTT	CCTTCTTCAC	CATGCATTTG	TTGACAGTAT	TTTTGAGCAG	TGGCTCCGAA	900
GGCACCGTCC	TCTTCAAGAA	GTTTATCCAG	AAGCCAATGC	ACCCATTGGA	CATAACCAGG	960
AATCCTACAT	GGTTCCTTTT	ATACCACTGT	ACAGAAATGG	TGATTTCTTT	ATTTCATCCA	1020
AAGATCTGGG	CTATGACTAT	AGCTATCTAC	AAGATTCAG			1059

- (2) INFORMATION FOR SEQ ID NO:60:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1587 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

ATGCTCCTGG CTGTTTTGTA	CTGCCTGCTG	TGGAGTTTCC	AGACCTCCGC	TGGCCATTTC	60
CCTAGAGCCT GTGTCTCCTC	TAAGAACCTG	ATGGAGAAGG	AATGCTGTCC	ACCGTGGAGC	120
GGGGACAGGA GTCCCTGTGG	CCAGCTTTCA	GGCAGAGGTT	CCTGTCAGAA	TATCCTTCTG	180
TCCAATGCAC CACTTGGGCC	TCAATTTCCC	TTCACAGGGG	TGGATGACCG	GGAGTCGTGG	240
CCTTCCGTCT TTTATAATAG	GACCTGCCAG	TGCTCTGGCA	ACTTCATGGG	ATTCAACTGT	300
GGAAACTGCA AGTTTGGCTT	TTGGGGACCA	AACTGCACAG	AGAGACGACT	CTTGGTGAGA	360
AGAAACATCT TCGATTTGAG	TGCCCCAGAG	AAGGACAAAT	TTTTTGCCTA	CCTCACTTTA	420
GCAAAGCATA CCATCAGCTC	AGACTATGTC	ATCCCCATAG	GGACCTATGG	CCAAATGAAA	480
AATGGATCAA CACCCATGTT	TAACGACATC	AATATTTATG	ACCTCTTTGT	CTGGATGCAT	540
TATTATGTGT CAATGGATGC	ACTGCTTGGG	GGATATGAAA	TCTGGAGAGA	CATTGATTTT	600
GCCCATGAAG CACCAGCTTT	TCTGCCTTGG	CATAGACTCT	TCTTGTTGCG	GTGGGAACAA	660
GAAATCCAGA AGCTGACAGG	AGATGAAAAC	TTCACTATTC	CATATTGGGA	CTGGCGGGAT	720
GCAGAAAAGT GTGACATTTG	CACAGATGAG	TACATGGGAG	GTCAGCACCC	CACAAATCCT	780
AACTTACTCA GCCCAGCATC	ATTCTTCTCC	TCTTGGCAGA	TTGTCTGTAG	CCGATTGGAG	840
GAGTACAACA GCCATCAGTC	TTTATGCAAT	GGAACGCCCG	AGGGACCTTT	ACGGCGTAAT	900
CCTGGAAACC ATGACAAATC	CAGAACCCCA	AGGCTCCCCT	CTTCAGCTGA	TGTAGAATTT	960
TGCCTGAGTT TGACCCAATA	TGAATCTGGT	TCCATGGATA	AAGCTGCCAA	TTTCAGCTTT	1020
AGAAATACAC TGGAAGGATT	TGCTAGTCCA	CTTACTGGGA	TAGCGGATGC	CTCTCAAAGC	1080
AGCATGCACA ATGCCTTGCA	CATCTATATG	AATGGAACAA	TGTCCCAGGT	ACAGGGATCT	1140
GCCAACGATC CTATCTTCCT	TCTTCACCAT	GCATTTGTTG	ACAGTATTTT	TGAGCAGTGG	1200
CTCCGAAGGC ACCGTCCTCT	TCAAGAAGTT	TATCCAGAAG	CCAATGCACC	CATTGGACAT	1260
AACCGGGAAT CCTACATGGT	TCCTTTTATA	CCACTGTACA	GAAATGGTGA	TTTCTTTATT	1320
TCATCCAAAG ATCTGGGCTA	TGACTATAGC	TATCTACAAG	ATTCAGACCC	AGACTCTTTT	1380
CAAGACTACA TTAAGTCCTA	TTTGGAACAA	GCGAGTCGGA	TCTGGTCATG	GCTCCTTGGG	1440
GCGGCGATGG TAGGGGCCGT	CCTCACTGCC	CTGCTGGCAG	GGCTTGTGAG	CTTGCTGTGT	1500
CGTCACAAGA GAAAGCAGCT	TCCTGAAGAA	AAGCAGCCAC	TCCTCATGGA	GAAAGAGGAT	1560
TACCACAGCT TGTATCAGAG	CCATTTA				1587

(2) INFORMATION FOR SEQ ID NO:61:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1587 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double

 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

ATGCTCCTGG	CTGTTTTGTA	CTGCCTGCTG	TGGAGTTTCC	AGACCTCCGC	TGGCCATTTC	60
CCTAGAGCCT	GTGTCTCCTC	TAAGAACCTG	ATGGAGAAGG	AATGCTGTCC	ACCGTGGAGC	120
GGGGACAGGA	GTCCCTGTGG	CCAGCTTTCA	GGCAGAGGTT	CCTGTCAGAA	TATCCTTCTG	180
TCCAATGCAC	CACTTGGGCC	TCAATTTCCC	TTCACAGGGG	TGGATGACCG	GGAGTCGTGG	240
CCTTCCGTCT	TTTATAATAG	GACCTGCCAG	TGCTCTGGCA	ACTTCATGGG	ATTCAACTGT	300
GGAAACTGCA	AGTTTGGCTT	TTGGGGACCA	AACTGCACAG	AGAGACGACT	CTTGGTGAGA	360
AGAAACATCT	TCGATTTGAG	TGCCCCAGAG	AAGGACAAAT	TTTTTGCCTA	CCTCACTTTA	420
GCAAAGCATA	CCATCAGCTC	AGACTATGTC	ATCCCCATAG	GGACCTATGG	CCAAATGAAA	480
AATGGATCAA	CACCCATGTT	TAACGACATC	AATATTTATG	ACCTCTTTGT	CTGGATGCAT	540
TATTATGTGT	CAATGGATGC	ACTGCTTGGG	GGATATGAAA	TCTGGAGAGA	CATTGATTTT	600
GCCCATGAAG	CACCAGCTTT	TCTGCCTTGG	CATAGACTCT	TCTTGTTGCG	GTGGGAACAA	660
GAAATCCAGA	AGCTGACAGG	AGATGAAAAC	TTCACTATTC	CATATTGGGA	CTGGCGGGAT	720
GCAGAAAAGT	GTGACATTTG	CACAGATGAG	TACATGGGAG	GTCAGCACCC	CACAAATCCT	780
AACTTACTCA	GCCCAGCATC	ATTCTTCTCC	TCTTGGCAGA	TTGTCTGTAG	CCGATTGGAG	840
GAGTACAACA	GCCATCAGTC	TTTATGCAAT	GGAACGCCCG	AGGGACCTTT	ACGGCGTAAT	900
CCTGGAAACC	ATGACAAATC	CAGAACCCCA	AGGCTCCCCT	CTTCAGCTGA	TGTAGAATTT	960
TGCCTGAGTT	TGACCCAATA	TGAATCTGGT	TCCATGGATA	AAGCTGCCAA	TTTCAGCTTT	1020
AGAAATACAC	TGGAAGGATT	TGCTAGTCCA	CTTACTGGGA	TAGCGGATGC	CTCTCAAAGC	1080
AGCATGCACA	ATGCCTTGCA	CATCTATATG	AATGGAACAA	TGTCCCAGGT	ACAGGGATCT	1140
GCCAACGATC	CTATCTTCCT	TCTTCACCAT	GCATTTGTTG	ACAGTATTTT	TGAGCAGTGG	1200
CTCCGAAGGC	ACCGTCCTCT	TCAAGAAGTT	TATCCAGAAG	CCAATGCACC	CATTGGACAT	1260
AACCAGGAAT	CCTACATGGT	TCCTTTTATA	CCACTGTACA	GAAATGGTGA	TTTCTTTATT	1320
TCATCCAAAG	ATCTGGGCTA	TGACTATAGC	TATCTACAAG	ATTCAGACCC	AGACTCTTTT	1380
CAAGACTACA	TTAAGTCCTA	TTTGGAACAA	GCGAGTCGGA	TCTGGTCATG	GCTCCTTGGG	1440

GCGGCGATGG TAGGGGCCGT CCTCACTGCC CTGCTGGCAG GGCTTGTGAG CTTGCTGTGT	1500
CGTCACAAGA GAAAGCAGCT TCCTGAAGAA AAGCAGCCAC TCCTCATGGA GAAAGAGGAT	1560
TACCACAGCT TGTATCAGAG CCATTTA	1587
(2) INFORMATION FOR SEQ ID NO:62:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 21 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
(ii) MOLECULE TYPE: DNA (genomic)	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:	
TAAATGGCTC TGATACAAGC T	21
(2) INFORMATION FOR SEQ ID NO:63:	
(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 20 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: single(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: DNA (genomic)	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:	
GCAAGTTTGG CTTTTGGGGA	20
(2) INFORMATION FOR SEQ ID NO:64:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 23 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
(ii) MOLECULE TYPE: DNA (genomic)	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:	
ATGCTCCTGG CTGTTTTGTA CTG	23
(2) INFORMATION FOR SEQ ID NO:65:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 157 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
(ii) MOLECULE TYPE: DNA (genomic)	

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:	
CTGAATCTTG TAGATAGCTA TAGTCATAGC CCAGATCTTT GGATGAAATA AAGAAATCAC	60
CATTTCTGTA CAGTGGTATA AAAGGAACCA TGTAGGATTC CCGGTTATGT CTAATGGGTG	120
CATTGGCTTC TGGATAAACT TCTTGAAGAG GACGGTG	157
(2) INFORMATION FOR SEQ ID NO:66:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 157 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
(ii) MOLECULE TYPE: DNA (genomic)	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:	
CTGAATCTTG TAGATAGCTA TAGTCATAGC CCAGATCTTT GGATGAAATA AAGAAATCAC	60
CATTTCTGTA CAGTGGTATA AAAGGAACCA TGTAGGATTC CTGGTTATGT CCAATGGGTG	120
CATTGGCTTC TGGATAAACT TCTTGAAGAG GACGGTG	157
(2) INFORMATION FOR SEQ ID NO:67:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 22 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
(ii) MOLECULE TYPE: DNA (genomic)	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:	
GGTTGGCCAA TCTACTCCCA GG	22
(2) INFORMATION FOR SEQ ID NO:68:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 20 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
(ii) MOLECULE TYPE: DNA (genomic)	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:	
GCTCACTCAG TGTGGCAAAG	20
(2) INFORMATION FOR SEQ ID NO:69:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 536 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	

- 45 -

- (ii) MOLECULE TYPE: DNA (genomic)
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

GGTTGGCCAA TCTACTCCCA GGAGCAGGGA GGGCAGGAGC CAGGGCTGGG CATAAAAGTC 60 AGGGCAGAGC CATCTATTGC TTACATTTGC TTCTGACACA ACTGTGTTCA CTAGCAACCT 120 CAAACAGACA CCATGGTGCA CCTGACTCCT GAGGAGAAGT CTGCCGTTAC TGCCCTGTGG 180 GGCAAGGTGA ACGTGGATGA AGTTGGTGGT GAGGCCCTGG GCAGGTTGGT ATCAAGGTTA 240 CAAGACAGGT TTAAGGAGAC CAATAGAAAC TGGGCATGTG GAGACAGAGA AGACTCTTGG 300 GTTTCTGATA GGCACTGACT CTCTCTGCCT ATTGGTCTAT TTTCCCACCC TTAGGCTGCT 360 GGTGGTCTAC CCTTGGACCC AGAGGTTCTT TGAGTCCTTT GGGGATCTGT CCACTCCTGA 420 TGCTGTTATG GGCAACCCTA AGGTGAAGGC TCATGGCAAG AAAGTGCTCG GTGCCTTTAG 480 TGATGGCCTG GCTCACCTGG ACAACCTCAA GGGCACCTTT GCCACACTGA GTGAGC 536

- (2) INFORMATION FOR SEQ ID NO:70:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 534 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

GGTTGGCCAA TCTACTCCCA GGAGCAGGGA GGGCAGGAGC CAGGGCTGGG CATAAAAGTC 60 AGGGCAGAGC CATCTATTGC TTACATTTGC TTCTGACACA ACTGTGTTCA CTAGCAACCT 120 CAAACAGACA CCATGGTGCA TCTGACTCCT GAGGAGGTCT GCCGTTACTG CCCTGTGGGG 180 CAAGGTGAAC GTGGATGAAG TTGGTGGTGA GGCCCTGGGC AGGTTGGTAT CAAGGTTACA 240 AGACAGGTTT AAGGAGACCA ATAGAAACTG GGCATGTGGA GACAGAGAAG ACTCTTGGGT 300 TTCTGATAGG CACTGACTCT CTCTGCCTAT TGGTCTATTT TCCCACCCTT AGGCTGCTGG 360 TGGTCTACCC TTGGACCCAG AGGTTCTTTG AGTCCTTTGG GGATCTGTCC ACTCCTGATG 420 CTGTTATGGG CAACCCTAAG GTGAAGGCTC ATGGCAAGAA AGTGCTCGGT GCCTTTAGTG 480 ATGGCCTGGC TCACCTGGAC AACCTCAAGG GCACCTTTGC CACACTGAGT GAGC 534

- (2) INFORMATION FOR SEQ ID NO:71:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 536 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)

(X1)	SEQUENCE	DESCRIPTION:	SEQ	תד	NO: 71:	
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GGTTGGCCAA	TCTACTCCCA	GGAGCAGGGA	GGGCAGGAGC	CAGGGCTGGG	CATAAAAGTC	60
AGGGCAGAGC	CATCTATTGC	TTACATTTGC	TTCTGACACA	ACTGTGTTCA	CTAGCAACCT	120
CAAACAGACA	CCATGGTGCA	CCTGACTCCT	GAGGAGAAGT	CTGCCGTTAC	TGCCCTGTGG	180
GGCAAGGTGA	ACGTGGATGA	AGTTGGTGGT	GAGGCCCTGG	GCAGGTTGGT	ATCAAGGTTA	240
CAAGACAGGT	TTAAGGAGAC	CAATAGAAAC	TGGGCATGTG	GAGACAGAGA	AGACTCTTGG	300
GTTTCTGATA	GGCACTGACT	CTCTCTGCCT	ATTGGTCTAT	TTTCCCACCC	TTAGGCTGCT	360
GGTGGTCTAC	CCTTGGACCT	AGAGGTTCTT	TGAGTCCTTT	GGGGATCTGT	CCACTCCTGA	420
TGCTGTTATG	GGCAACCCTA	AGGTGAAGGC	TCATGGCAAG	AAAGTGCTCG	GTGCCTTTAG	480
TGATGGCCTG	GCTCACCTGG	ACAACCTCAA	GGGCACCTTT	GCCACACTGA	GTGAGC	536

(2) INFORMATION FOR SEQ ID NO:72:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 536 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

GGTTGGCCAA	TCTACTCCCA	GGAGCAGGGA	GGGCAGGAGC	CAGGGCTGGG	CATAAAAGTC	60
AGGGCAGAGC	CATCTATTGC	TTACATTTGC	TTCTGACACA	ACTGTGTTCA	CTAGCAACCT	120
CAAACAGACA	CCATGGTGCA	CCTGACTCCT	GAGGAGAAGT	CTGCCGTTAC	TGCCCTGTGG	180
GGCAAGGTGA	ACGTGGATGA	AGTTGGAGGT	GAGGCCCTGG	GCAGGTTGGT	ATCAAGGTTA	240
CAAGACAGGT	TTAAGGAGAC	CAATAGAAAC	TGGGCATGTG	GAGACAGAGA	AGACTCTTGG	300
GTTTCTGATA	GGCACTGACT	CTCTCTGCCT	ATTGGTCTAT	TTTCCCACCC	TTAGGCTGCT	360
GGTGGTCTAC	CCTTGGACCC	AGAGGTTCTT	TGAGTCCTTT	GGGGATCTGT	CCACTCCTGA	420
TGCTGTTATG	GGCAACCCTA	AGGTGAAGGC	TCATGGCAAG	AAAGTGCTCG	GTGCCTTTAG	480
TGATGGCCTG	GCTCACCTGG	ACAACCTCAA	GGGCACCTTT	GCCACACTGA	GTGAGC	536

(2) INFORMATION FOR SEQ ID NO:73:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 64 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: RNA (genomic)

351

ATTTTAGAAG TAGGCCAGTG TGTGTTCCCA TCTCTCCTAG CCGCCGCCTG G

(2)	INFORMATION	FOR	SEQ	ID	NO:77:
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- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 340 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

GGCTGACAAG AAGGAAACTC GCTGAGATAG CAGGGACTTT CCACAAGGGG ATGTTATGGG 60
GAGGAGCCGG TCGGGAACAC CCACTTTCTT GATGTATAAA TATCACTGCA TTTCGCTCTG 120
TATTCAGTCG CTCTGCGGAG AGGCTGGCAG ATTGAGCCCT GGGAGGTTCT CTCCAGCACT 180
AGCAGGTAGA GCCTGGGTGT TCCCTGCTAG ACTCTCACCA GCACTTAGCC AGTGCTGGGC 240
AGAGTGGCTC CACGCTTGCT TGCTTAAAGA CCTCTTCAAT AAAGCTGCCA TTTTAGAAGT 300
AAGCCAGTGT GTGTTCCCAT CTCTCCTAGC CGCCGCCTGG 340

(2) INFORMATION FOR SEQ ID NO:78:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 340 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

GGCTGACAAG AAGGAAACTC GCTGAGATAG CAGGGACTTT CCACAAGGGG ATGTTATGGG 60
GAGGAGCCGG TCGGGAACAC CCACTTTCTT GGTGTATAAA TATCACTGCA TTTCGCTCTG 120
TATTCAGTCG CTCTGCGGAG AGGCTGGCAG ATTGAGCCCT GGGAGGTTCT CTCCAGCACT 180
AGCAGGTAGA GCCTGGGTGT TCCCTGCTAG ACTCTCACCA GCACTTGGCC AGTGCTGGGC 240
AGAGTGGCTC CACGCTTGCT TGCTTAAAGA CCTCTTCAAT AAAGCTGCCA TTTTAGAAGT 300
AAGCCAGTGT GTGTTCCCAT CTCTCCTAGC CGCCGCCTGG

(2) INFORMATION FOR SEO ID NO:79:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 351 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)

60

GAGGTACTGG GGAGGAGCCG GTCGGGAACG CCCCCTCTCT TGATGTATAA ATATCACTGC	120
ATTTCGCTCT GTATTCAGTC GCTCTGCGGA GAGGCTGGCA GATTGAGCCC TGGGAGGTTC	180
TCTCCAGCAC TAGCAGGTAG AGCCTGGGTG TTCCCTGCTA GACTCTCACC AGCACTTGGC	240
CGGTGCTGGG CAGAGTGGCT CCACGCTTGC TTGCTTAAAG ACCTCTTCAA TAAAGCTGCC	300
ATTTTAGAAG TAGGCTAGTG TGTGTTCCCA TCTCTCCTAG CCGCCGCCTG G	351
(2) INFORMATION FOR SEQ ID NO:80:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 351 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
(ii) MOLECULE TYPE: DNA (genomic)	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:	
GGCTGACAAG AAGGAAACTC GCTGAAACAG CAGGGACTTT CCACAAGGGG ATGTTACGGG	60
GAGGTACTGG GAAGGAGCCG GTCGGGAACG CCCACTTTCT TGATGTATAA ATATCACTGC	120
ATTTCGCTCT GTATTCAGTC GCTCTGCGGA GAGGCTGGCA GATTGAGCCC TGGGAGGTTC	180
TCTCCAGCAC TAGCAGGTAG AGCCTGGGTG TTCCCTGCTA GACTCTCACC AGCACTTGGC	240
CGGTGCTGGG CAGAGTGACT CCACGCTTGC TTGCTTAAAG CCCTCTTCAA TAAAGCTGCC	300
ATTTTAGAAG TAAGCTAGTG TGTGTTCCCA TCTCTCCTAG CCGCCGCCTG G	351
(2) INFORMATION FOR SEQ ID NO:81:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 351 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
(ii) MOLECULE TYPE: DNA (genomic)	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:	
GGCTGACAAG AAGGAAACTC GCTGAGACAG CAGGGACTTT CCACAAGGGG ATGTTACGGA	60
GAGGTACTGG GGAGGAGCCG GTCGGGAACG CCCACTCTCT TGATGTATAA ATATCACTGC	120
ATTTCGCTCT GTATTCAGTC GCTCTGCGGA GAGGCTGGCA GATTGAGCCC TAGGAGGTTC	180
TCTCCAGCAC TAGCAGGTAG AGCCTGAGTG TTCCCTGCTA AACTCTCACC AGCACTTGGC	240
CGGTGCTGGG CAGAGCGGCT CCACGCTTGC TTGCTTAAAG ACCTCTTCAA TAAAGCTGCC	300
ATTTTAGAAG TAGGCTAGTG TGTGTTCCCA TCTCTCCTAG CCGCCGCCTG G	351

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:

GGCTGACAAG AAGGAAACTC GCTGAGACAG CAGGGACTTT CCACAAGGGG ATGTTACGGG

(2) INFORMATION FOR SEQ ID NO:82:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 536 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:

GGTTGGCCAA	TCTACTCCCA	GGAGCAGGGA	GGGCAGGAGC	CAGGGCTGGG	CATAAAAGTC	60
AGGGCAGAGC	CATCTATTGC	TTACATTTGC	TTCTGACACA	ACTGTGTTCA	CTAGCAACCT	120
CAAACAGACA	CCATGGTGCA	TCTGACTCCT	GAGGAGAAGT	CTGCCGTTAC	TGCCCTGTGG	180
GGCAAGGTGA	ACGTGGATGA	AGTTGGTGGT	AAGGCCCTGG	GCAGGTTGGT	ATCAAGGTTA	240
CAAGACAGGT	TTAAGGAGAC	CAATAGAAAC	TGGGCATGTG	GAGACAGAGA	AGACTCTTGG	300
GTTTCTGATA	GGCACTGACT	CTCTCTGCCT	ATTGGTCTAT	TTTCCCACCC	TTAGGCTGCT	360
GGTGGTCTAC	CCTTGGACCC	AGAGGTTCTT	TGAGTCCTTT	GGGGATCTGT	CCACTCCTGA	420
TGCTGTTATG	GGCAACCCTA	AGGTGAAGGC	TCATGGCAAG	AAAGTGCTCG	GTGCCTTTAG	480
TGATGGCCTG	GCTCACCTGG	ACAACCTCAA	GGGCACCTTT	GCCACACTGA	GTGAGC	536

(2) INFORMATION FOR SEQ ID NO:83:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 536 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:

GGTTGGCCAA	TCTACTCCCA	GGAGCAGGGA	GGGCAGGAGC	CAGGGCTGGG	CATAAAAGTC	60
AGGGCAGAGC	CATCTATTGC	TTACATTTGC	TTCTGACACA	ACTGTGTTCA	CTAGCAACCT	120
CAAACAGACA	CCATGGTGCA	CCTGACTCCT	GAGGAGAAGT	CTGCCGTTAC	TGCCCTGTGG	180
GGCAAGGTGA	ACGTGGATGA	AGTTGGTGGT	GAGGCCCTGG	GCAGGTTGGT	ATCAAGGTTA	240
CAAGACAGGT	TTAAGGAGAC	CAATAGAAAC	TGGGCATGTG	GAGACAGAGA	AGACTCTTGG	300
GTTTCTGATA	GGCACTGACT	CTCTCTGCCT	ATTAGTCTAT	TTTCCCACCC	TTAGGCTGCT	360
GGTGGTCTAC	CCTTGGACCC	AGAGGTTCTT	TGAGTCCTTT	GGGGATCTGT	CCACTCCTGA	420
TGCTGTTATG	GGCAACCCTA	AGGTGAAGGC	TCATGGCAAG	AAAGTGCTCG	GTGCCTTTAG	480
TGATGGCCTG	GCTCACCTGG	ACAACCTCAA	GGGCACCTTT	GCCACACTGA	GTGAGC	536

60

120

157

(2)	INFO	RMAT:	ION 1	FOR 8	SEQ :	ID NO	0:84	:								
	(i)	(A) (B) (C)	LEI TYI STI	NGTH PE: 1 RAND	ARAC' : 15' nucle EDNES	7 bas eic a SS: 0	se pa acid doub!	airs								
	(ii)	MOLI	ECULI	E TYI	PE: I	ANC	(gend	omic))							
	(xi)	SEQ	JENCI	E DES	SCRI	PTIO	1: S1	EQ II	ои с	:84:						
CACC	GTCC1	rc T	rcaa(GAAG:	r tta	ATCC	AGAA	GCC	AATG	CAC (CCAT	rgga	CA TA	AACC	AGGA	A
TCCT	ACATO	3G T	rcct:	TTTA:	r ac	CACTO	STAC	AGA	AATGO	GTG A	TTT	CTTT	AT T	CAT	CCAA	Ą
GATC	TGGG	CT A	rgac'	(ATA	G CTA	ATCT	ACAA	GAT	rcag							
(2)	INFOR	RMAT:	ION I	FOR S	SEQ I	ID NO	0:85	:								
	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 833 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 															
	(ii)	MOLI	ECULI	TYI	PE: 1	prote	ein									
	(xi)	SEQU	JENCI	E DES	SCRII	PTIO	1: SI	EQ II	ONO.	:85:						
	Met 1	Asn	Ser	Gly	Met 5	Leu	Pro	Leu	Phe	Glu 10	Pro	Lys	Gly	Arg	Val 15	Leu
	Leu	Val	Asp	Gly 20	His	His	Leu	Ala	Tyr 25	Arg	Thr	Phe	His	Ala 30	Leu	Lys
	Gly	Leu	Thr 35	Thr	Ser	Arg	Gly	Glu 40	Pro	Val	Gln	Ala	Val 45	Tyr	Gly	Phe
	Ala	Lys 50	Ser	Leu	Leu	Lys	Ala 55	Leu	Lys	Glu	Asp	Gly 60	Asp	Ala	Val	Ile
	Val 65	Val	Phe	Asp	Ala	Lys 70	Ala	Pro	Ser	Phe	Arg 75	His	Glu	Ala	Tyr	Gly 80
	Gly	Tyr	Lys	Ala	Gly 85	Arg	Ala	Pro	Thr	Pro 90	Glu	Asp	Phe	Pro	Arg 95	Gln
	Leu	Ala	Leu	Ile 100	Lys	Glu	Leu	Val	Asp 105	Leu	Leu	Gly	Leu	Ala 110	Arg	Leu
	Glu	Val	Pro 115	Gly	Tyr	Glu	Ala	Asp 120	Asp	Val	Leu	Ala	Ser 125	Leu	Ala	Lys
	Lys	Ala 130	Glu	Lys	Glu	Gly	Tyr 135	Glu	Val	Arg	Ile	Leu 140	Thr	Ala	Asp	Lys
	Asp 145	Leu	Tyr	Gln	Leu	Leu 150	Ser	Asp	Arg	Ile	His 155	Val	Leu	His	Pro	Glu 160
	Gly	Tyr	Leu	Ile	Thr 165	Pro	Ala	Trp	Leu	Trp 170	Glu	Lys	Tyr	Gly	Leu 175	Arg

Pro Asp Gln Trp Ala Asp Tyr Arg Ala Leu Thr Gly Asp Glu Ser Asp 180 Asn Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Arg Lys Leu 195 200 Leu Glu Glu Trp Gly Ser Leu Glu Ala Leu Leu Lys Asn Leu Asp Arg 210 215 Leu Lys Pro Ala Ile Arg Glu Lys Ile Leu Ala His Met Asp Asp Leu 225 230 235 Lys Leu Ser Trp Asp Leu Ala Lys Val Arg Thr Asp Leu Pro Leu Glu 245 250 Val Asp Phe Ala Lys Arg Arg Glu Pro Asp Arg Glu Arg Leu Arg Ala 265 Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly Leu 280 Leu Glu Ser Pro Lys Ala Leu Glu Glu Ala Pro Trp Pro Pro Pro Glu 295 Gly Ala Phe Val Gly Phe Val Leu Ser Arg Lys Glu Pro Met Trp Ala 310 315 Asp Leu Leu Ala Leu Ala Ala Ala Arg Gly Gly Arg Val His Arg Ala 330 325 Pro Glu Pro Tyr Lys Ala Leu Arg Asp Leu Lys Glu Ala Arg Gly Leu 340 345 350 Leu Ala Lys Asp Leu Ser Val Leu Ala Leu Arg Glu Gly Leu Gly Leu 355 360 Pro Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Asp Pro Ser 370 375 380 Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Trp Thr 385 390 Glu Glu Ala Gly Glu Arg Ala Ala Leu Ser Glu Arg Leu Phe Ala Asn 405 410 Leu Trp Gly Arg Leu Glu Gly Glu Glu Arg Leu Leu Trp Leu Tyr Arg 425 Glu Val Glu Arg Pro Leu Ser Ala Val Leu Ala His Met Glu Ala Thr 440 445 Gly Val Arg Leu Asp Val Ala Tyr Leu Arg Ala Leu Ser Leu Glu Val 455 460 Ala Gly Glu Ile Ala Arg Leu Glu Ala Glu Val Phe Arg Leu Ala Gly 475 His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Leu Phe 485 Asp Glu Leu Gly Leu Pro Ala Ile Gly Lys Thr Glu Lys Thr Gly Lys

Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu Ala His Pro 515 Ile Val Glu Lys Ile Leu Gln Tyr Arg Glu Leu Thr Lys Leu Lys Ser 535 Thr Tyr Ile Asp Pro Leu Pro Asp Leu Ile His Pro Arg Thr Gly Arg 545 550 560 Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg Leu Ser 565 575 Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro Leu Gly 580 585 Gln Arg Ile Arg Arg Ala Phe Ile Ala Glu Glu Gly Trp Leu Leu Val 600 Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu Ser 615 Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Arg Asp Ile His Thr Glu Thr Ala Ser Trp Met Phe Gly Val Pro Arg Glu Ala Val Asp 650 Pro Leu Met Arg Arg Ala Ala Lys Thr Ile Asn Phe Gly Val Leu Tyr 660 665 Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile Pro Tyr Glu 675 680 Glu Ala Gln Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe Pro Lys Val 690 695 Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Arg Gly Tyr 710 705 715 Val Glu Thr Leu Phe Gly Arg Arg Tyr Val Pro Asp Leu Glu Ala 725 730 Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn Met 740 745 Pro Val Arg Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val Lys 760 Leu Phe Pro Arg Leu Glu Glu Met Gly Ala Arg Met Leu Leu Gln Val 775 His Asp Glu Leu Val Leu Glu Ala Pro Lys Glu Arg Ala Glu Ala Val 790 795 Ala Arg Leu Ala Lys Glu Val Met Glu Gly Val Tyr Pro Leu Ala Val Pro Leu Glu Val Glu Val Gly Ile Gly Glu Asp Trp Leu Ser Ala Lys 825

Glu

(2) INFORMATION FOR SEQ ID NO:86:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 548 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:
- Met Asn Ser Gly Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val Leu
 1 5 10 15
- Leu Val Asp Gly His His Leu Ala Tyr Arg Thr Phe His Ala Leu Lys
 20 25 30
- Gly Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly Phe
 35 40 45
- Ala Lys Ser Leu Lys Ala Leu Lys Glu Asp Gly Asp Ala Val Ile 50 55
- Val Val Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala Tyr Gly 75 75 80
- Gly Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln 85 90 95
- Leu Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Leu Ala Arg Leu 100 105 110
- Glu Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Ser Leu Ala Lys 115 120 125
- Lys Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp Lys 130 135 140
- Asp Leu Tyr Gln Leu Leu Ser Asp Arg Ile His Val Leu His Pro Glu
 145 150 155 160
- Gly Tyr Leu Ile Thr Pro Ala Trp Leu Trp Glu Lys Tyr Gly Leu Arg 165 170 175
- Pro Asp Gln Trp Ala Asp Tyr Arg Ala Leu Thr Gly Asp Glu Ser Asp 180 185 190
- Asn Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Arg Lys Leu 195 200 205
- Leu Glu Glu Trp Gly Ser Leu Glu Ala Leu Leu Lys Asn Leu Asp Arg 210 215 220
- Leu Lys Pro Ala Ile Arg Glu Lys Ile Leu Ala His Met Asp Asp Leu 225 230 235 240
- Lys Leu Ser Trp Asp Leu Ala Lys Val Arg Thr Asp Leu Pro Leu Glu 245 250 255
- Val Asp Phe Ala Lys Arg Arg Glu Pro Asp Arg Glu Arg Leu Arg Ala 260 265 270

Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly Leu 275 Leu Glu Ser Pro Lys Ala Leu Glu Glu Ala Pro Trp Pro Pro Glu 290 295 300 Gly Ala Phe Val Gly Phe Val Leu Ser Arg Lys Glu Pro Met Trp Ala 305 310 315 320 Asp Leu Leu Ala Leu Ala Ala Ala Arg Gly Gly Arg Val His Arg Ala 325 330 Pro Glu Pro Tyr Lys Ala Leu Arg Asp Leu Lys Glu Ala Arg Gly Leu 340 345 Leu Ala Lys Asp Leu Ser Val Leu Ala Leu Arg Glu Gly Leu Gly Leu 360 Pro Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Asp Pro Ser 375 Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Trp Thr 395 Glu Glu Ala Gly Glu Arg Ala Ala Leu Ser Glu Arg Leu Phe Ala Asn 405 Leu Trp Gly Arg Leu Glu Glu Glu Arg Leu Leu Trp Leu Tyr Arg 420 425 Glu Val Glu Arg Pro Leu Ser Ala Val Leu Ala His Met Glu Ala Thr 435 445 Gly Val Arg Leu Asp Val Ala Tyr Leu Arg Ala Leu Ser Leu Glu Val 450 455 460 Ala Gly Glu Ile Ala Arg Leu Glu Ala Glu Val Phe Arg Leu Ala Gly 465 470 475 480 His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Leu Phe 485 490 Asp Glu Leu Gly Leu Pro Ala Ile Gly Lys Thr Glu Lys Thr Gly Lys 505 510 Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu Ala His Pro 515 520 Ile Val Glu Lys Ile Leu Gln Ala Cys Lys Leu Gly Thr Gly Arg Arg 535 540

(2) INFORMATION FOR SEQ ID NO:87:

Phe Thr Thr Ser

545

- (i) SEOUENCE CHARACTERISTICS:
 - (A) LENGTH: 695 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:

Met Asn Ser Gly Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val Leu
1 5 10 15

Leu Val Asp Gly His His Leu Ala Tyr Arg Thr Phe His Ala Leu Lys
20 25 30

Gly Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly Phe 35 40 45

Ala Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Asp Ala Val Ile 50 60

Val Val Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala Tyr Gly
65 70 75 80

Gly Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln 85 90 95

Leu Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Leu Ala Arg Leu 100 105 110

Glu Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Ser Leu Ala Lys 115 120 125

Lys Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp Lys 130 135 140

Asp Leu Tyr Gln Leu Leu Ser Asp Arg Ile His Val Leu His Pro Glu 145 150 155

Gly Tyr Leu Ile Thr Pro Ala Trp Leu Trp Glu Lys Tyr Gly Leu Arg 165 170 175

Pro Asp Gln Trp Ala Asp Tyr Arg Ala Leu Thr Gly Asp Glu Ser Asp 180 185 190

Asn Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Arg Lys Leu 195 200 205

Leu Glu Glu Trp Gly Ser Leu Glu Ala Leu Leu Lys Asn Leu Asp Arg 210 215 220

Leu Lys Pro Ala Ile Arg Glu Lys Ile Leu Ala His Met Asp Asp Leu 225 230 235

Lys Leu Ser Trp Asp Leu Ala Lys Val Arg Thr Asp Leu Pro Leu Glu 245 250 255

Val Asp Phe Ala Lys Arg Arg Glu Pro Asp Arg Glu Arg Leu Arg Ala 260 265 270

Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly Leu 275 280 285

Leu Glu Ser Pro Lys Ala Leu Glu Glu Ala Pro Trp Pro Pro Pro Glu 290 295 300 Gly Ala Phe Val Gly Phe Val Leu Ser Arg Lys Glu Pro Met Trp Ala Asp Leu Leu Ala Leu Ala Ala Ala Arg Gly Gly Arg Val His Arg Ala Pro Glu Pro Tyr Lys Ala Leu Arg Asp Leu Lys Glu Ala Arg Gly Leu Leu Ala Lys Asp Leu Ser Val Leu Ala Leu Arg Glu Gly Leu Gly Leu Pro Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Asp Pro Ser Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Trp Thr Glu Glu Ala Gly Glu Arg Ala Ala Leu Ser Glu Arg Leu Phe Ala Asn Leu Trp Gly Arg Leu Glu Gly Glu Glu Arg Leu Leu Trp Leu Tyr Arg Glu Val Glu Arg Pro Leu Ser Ala Val Leu Ala His Met Glu Ala Thr Gly Val Arg Leu Asp Val Ala Tyr Leu Arg Ala Leu Ser Leu Glu Val Ala Gly Glu Ile Ala Arg Leu Glu Ala Glu Val Phe Arg Leu Ala Gly His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Leu Phe Asp Glu Leu Gly Leu Pro Ala Ile Gly Lys Thr Glu Lys Thr Gly Lys Arq Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu Ala His Pro Ile Val Glu Lys Ile Leu Gln Tyr Arg Glu Leu Thr Lys Leu Lys Ser Thr Tyr Ile Asp Pro Leu Pro Asp Leu Ile His Pro Arg Thr Gly Arg Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg Leu Ser Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro Leu Gly Gln Arg Ile Arg Arg Ala Phe Ile Ala Glu Glu Gly Trp Leu Leu Val Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu Ser Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Arg Asp Ile His

Thr Glu Thr Ala Ser Trp Met Phe Gly Val Pro Arg Glu Ala Val Asp 645 650 655

Pro Leu Met Arg Arg Ala Ala Lys Thr Ile Asn Phe Gly Val Leu Tyr 660 665 670

Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ser His Pro Leu 675 680 685

Arg Gly Gly Pro Gly Leu His 690 695

(2) INFORMATION FOR SEQ ID NO:88:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 310 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:

Met Asn Ser Gly Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val Leu 1 5 10 15

Leu Val Asp Gly His His Leu Ala Tyr Arg Thr Phe His Ala Leu Lys
20 25 30

Gly Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly Phe 35 40 45

Ala Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Asp Ala Val Ile 50 55 60

Val Val Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala Tyr Gly 70 75 80

Gly Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln 85 90 95

Leu Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Leu Ala Arg Leu 100 105 110

Glu Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Ser Leu Ala Lys 115 120 125

Lys Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp Lys
130 135 140

Asp Leu Tyr Gln Leu Leu Ser Asp Arg Ile His Val Leu His Pro Glu 145 150 155 160

Gly Tyr Leu Ile Thr Pro Ala Trp Leu Trp Glu Lys Tyr Gly Leu Arg 165 170 175

Pro Asp Gln Trp Ala Asp Tyr Arg Ala Leu Thr Gly Asp Glu Ser Asp 180 185 190

Asn Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Arg Lys Leu 195 200 205 Leu Glu Glu Trp Gly Ser Leu Glu Ala Leu Leu Lys Asn Leu Asp Arg 210 215 220

Leu Lys Pro Ala Ile Arg Glu Lys Ile Leu Ala His Met Asp Asp Leu 225 230 235

Lys Leu Ser Trp Asp Leu Ala Lys Val Arg Thr Asp Leu Pro Leu Glu 245 250 255

Val Asp Phe Ala Lys Arg Arg Glu Pro Asp Arg Glu Arg Leu Arg Ala 260 265 270

Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly Leu 275 280 285

Leu Glu Ser Pro Lys Ser Trp Arg Gly Cys Ile Pro Trp Pro Cys Pro 290 295 300

Trp Arg Trp Arg Trp Gly 305

(2) INFORMATION FOR SEQ ID NO:89:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 322 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:89:

Met Ala Ser Met Thr Gly Gly Gln Gln Met Gly Arg Ile Asn Ser Gly 1 5 10 15

Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val Leu Leu Val Asp Gly 20 25 30

His His Leu Ala Tyr Arg Thr Phe His Ala Leu Lys Gly Leu Thr Thr 35 40 45

Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly Phe Ala Lys Ser Leu 50 60

Leu Lys Ala Leu Lys Glu Asp Gly Asp Ala Val Ile Val Val Phe Asp 65 70 75 80

Ala Lys Ala Pro Ser Phe Arg His Glu Ala Tyr Gly Gly Tyr Lys Ala 85 90 95

Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln Leu Ala Leu Ile 100 105 110

Lys Glu Leu Val Asp Leu Leu Gly Leu Ala Arg Leu Glu Val Pro Gly 115 120 125

Tyr Glu Ala Asp Asp Val Leu Ala Ser Leu Ala Lys Lys Ala Glu Lys 130 135 140

Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp Lys Asp Leu Tyr Gln 145 150 155 160 Leu Leu Ser Asp Arg Ile His Val Leu His Pro Glu Gly Tyr Leu Ile 165 170 175

Thr Pro Ala Trp Leu Trp Glu Lys Tyr Gly Leu Arg Pro Asp Gln Trp
180 185 190

Ala Asp Tyr Arg Ala Leu Thr Gly Asp Glu Ser Asp Asn Leu Pro Gly 195 200 205

Val Lys Gly Ile Gly Glu Lys Thr Ala Arg Lys Leu Leu Glu Glu Trp 210 225

Gly Ser Leu Glu Ala Leu Leu Lys Asn Leu Asp Arg Leu Lys Pro Ala 235 230 240

Ile Arg Glu Lys Ile Leu Ala His Met Asp Asp Leu Lys Leu Ser Trp 245 250 255

Asp Leu Ala Lys Val Arg Thr Asp Leu Pro Leu Glu Val Asp Phe Ala 260 270

Lys Arg Arg Glu Pro Asp Arg Glu Arg Leu Arg Ala Phe Leu Glu Arg 275 280 285

Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly Leu Leu Glu Ser Pro 290 295 300

Lys Ser Trp Arg Gly Cys Ile Pro Trp Pro Cys Pro Trp Arg Trp Arg 305 310 315

Trp Gly

(2) INFORMATION FOR SEQ ID NO:90:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 528 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:90:

Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val Leu Leu Val Asp Gly
1 5 10 15

His His Leu Ala Tyr Arg Thr Phe His Ala Leu Lys Gly Leu Thr Thr 20 25 30

Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly Phe Ala Lys Ser Leu 35 40 45

Leu Lys Ala Leu Lys Glu Asp Gly Asp Ala Val Ile Val Val Phe Asp 50 60

Ala Lys Ala Pro Ser Phe Arg His Glu Ala Tyr Gly Gly Tyr Lys Ala 65 70 75 80

Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln Leu Ala Leu Ile 85 90 95

Lys Glu Leu Val Asp Leu Leu Gly Leu Ala Arg Leu Glu Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Ser Leu Ala Lys Lys Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp Lys Asp Leu Tyr Gln Leu Leu Ser Asp Arg Ile His Val Leu His Pro Glu Gly Tyr Leu Ile Thr Pro Ala Trp Leu Trp Glu Lys Tyr Gly Leu Arg Pro Asp Gln Trp Ala Asp Tyr Arg Ala Leu Thr Gly Asp Glu Ser Asp Asn Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Arg Lys Leu Leu Glu Glu Trp Gly Ser Leu Glu Ala Leu Leu Lys Asn Leu Asp Arg Leu Lys Pro Ala Ile Arg Glu Lys Ile Leu Ala His Met Asp Asp Leu Lys Leu Ser Trp Asp Leu Ala Lys Val Arg Thr Asp Leu Pro Leu Glu Val Asp Phe Ala Lys Arg Arg Glu Pro Asp Arg Glu Arg Leu Arg Ala Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly Leu Leu Glu Ser Pro Lys Ile Arg Arg Ala Phe Ile Ala Glu Glu Gly Trp Leu Leu Val Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu Ser Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Arg Asp Ile His Thr Glu Thr Ala Ser Trp Met Phe Gly Val Pro Arg Glu Ala Val Asp Pro Leu Met Arg Arg Ala Ala Lys Thr Ile Asn Phe Gly Val Leu Tyr Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile Pro Tyr Glu Glu Ala Gln Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe Pro Lys Val Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Arg Arg Gly Tyr Val Glu Thr Leu Phe Gly Arg Arg Tyr Val Pro Asp Leu Glu Ala Arg

Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn Met Pro 435 440 445

Val Arg Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val Lys Leu 450 460

Phe Pro Arg Leu Glu Glu Met Gly Ala Arg Met Leu Leu Gln Val His 465 470 475 480

Asp Glu Leu Val Leu Glu Ala Pro Lys Glu Arg Ala Glu Ala Val Ala 485 490 495

Arg Leu Ala Lys Glu Val Met Glu Gly Val Tyr Pro Leu Ala Val Pro 500 510

Leu Glu Val Glu Val Gly Ile Gly Glu Asp Trp Leu Ser Ala Lys Glu 515 520 525

(2) INFORMATION FOR SEQ ID NO:91:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 315 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:91:

Met Ala Ser Met Thr Gly Gly Gln Gln Met Gly Arg Ile Asn Ser Gly
1 10 15

Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val Leu Leu Val Asp Gly 20 25 30

His His Leu Ala Tyr Arg Thr Phe His Ala Leu Lys Gly Leu Thr Thr 35 40 45

Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly Phe Ala Lys Ser Leu 50

Leu Lys Ala Leu Lys Glu Asp Gly Asp Ala Val Ile Val Val Phe Asp 65 70 75 80

Ala Lys Ala Pro Ser Phe Arg His Glu Ala Tyr Gly Gly Tyr Lys Ala 85 90 95

Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln Leu Ala Leu Ile 100 105 110

Lys Glu Leu Val Asp Leu Leu Gly Leu Ala Arg Leu Glu Val Pro Gly 115 120 125

Tyr Glu Ala Asp Asp Val Leu Ala Ser Leu Ala Lys Lys Ala Glu Lys 130 135 140

Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp Lys Asp Leu Tyr Gln 145 150 155 Leu Leu Ser Asp Arg Ile His Val Leu His Pro Glu Gly Tyr Leu Ile 165 170 Thr Pro Ala Trp Leu Trp Glu Lys Tyr Gly Leu Arg Pro Asp Gln Trp 180 185 Ala Asp Tyr Arg Ala Leu Thr Gly Asp Glu Ser Asp Asn Leu Pro Gly 195 200 205 Val Lys Gly Ile Gly Glu Lys Thr Ala Arg Lys Leu Leu Glu Glu Trp 210 215 220 Gly Ser Leu Glu Ala Leu Leu Lys Asn Leu Asp Arg Leu Lys Pro Ala 225 230 Ile Arg Glu Lys Ile Leu Ala His Met Asp Asp Leu Lys Leu Ser Trp 245 250 Asp Leu Ala Lys Val Arg Thr Asp Leu Pro Leu Glu Val Asp Phe Ala 260 265 Lys Arg Arg Glu Pro Asp Arg Glu Arg Leu Arg Ala Phe Leu Glu Arg 280 Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly Leu Leu Glu Ser Pro 295 Lys Ala Ala Leu Glu His His His His His 305 310

- (2) INFORMATION FOR SEQ ID NO:92:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1182 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:

ATGGAGGAGC	CGCAGTCAGA	TCCTAGCGTC	GAGCCCCCTC	TGAGTCAGGA	AACATTTTCA	60
GACCTATGGA	AACTACTTCC	TGAAAACAAC	GTTCTGTCCC	CCTTGCCGTC	CCAAGCAATG	120
GATGATTTGA	TGCTGTCCCC	GGACGATATT	GAACAATGGT	TCACTGAAGA	CCCAGGTCCA	180
GATGAAGCTC	CCAGAATGCC	AGAGGCTGCT	CCCCCGTGG	CCCCTGCACC	AGCAGCTCCT	240
ACACCGGCGG	CCCCTGCACC	AGCCCCCTCC	TGGCCCCTGT	CATCTTCTGT	CCCTTCCCAG	300
AAAACCTACC	AGGGCAGCTA	CGGTTTCCGT	CTGGGCTTCT	TGCATTCTGG	GACAGCCAAG	360
TCTGTGACTT	GCACGTACTC	CCCTGCCCTC	AACAAGATGT	TTTGCCAACT	GGCCAAGACC	420
TGCCCTGTGC	AGCTGTGGGT	TGATTCCACA	CCCCCGCCCG	GCACCCGCGT	CCGCGCCATG	480
GCCATCTACA	AGCAGTCACA	GCACATGACG	GAGGTTGTGA	GGCGCTGCCC	CCACCATGAG	540
CGCTGCTCAG	ATAGCGATGG	TCTGGCCCCT	CCTCAGCATC	TTATCCGAGT	GGAAGGAAAT	600

D9940925.O61002

TTGCGTGTGG	AGTATTTGGA	TGACAGAAAC	ACTTTTCGAC	ATAGTGTGGT	GGTGCCCTAT	660
GAGCCGCCTG	AGGTTGGCTC	TGACTGTACC	ACCATCCACT	ACAACTACAT	GTGTAACAGT	720
TCCTGCATGG	GCGGCATGAA	CCGGAGGCCC	ATCCTCACCA	TCATCACACT	GGAAGACTCC	780
AGTGGTAATC	TACTGGGACG	GAACAGCTTT	GAGGTGCGTG	TTTGTGCCTG	TCCTGGGAGA	840
GACCGGCGCA	CAGAGGAAGA	GAATCTCCGC	AAGAAAGGGG	AGCCTCACCA	CGAGCTGCCC	900
CCAGGGAGCA	CTAAGCGAGC	ACTGCCCAAC	AACACCAGCT	CCTCTCCCCA	GCCAAAGAAG	960
AAACCACTGG	ATGGAGAATA	TTTCACCCTT	CAGATCCGTG	GGCGTGAGCG	CTTCGAGATG	1020
TTCCGAGAGC	TGAATGAGGC	CTTGGAACTC	AAGGATGCCC	AGGCTGGGAA	GGAGCCAGGG	1080
GGGAGCAGGG	CTCACTCCAG	CCACCTGAAG	TCCAAAAAGG	GTCAGTCTAC	CTCCCGCCAT	1140
AAAAAACTCA	TGTTCAAGAC	AGAAGGCCT	GACTCAGACT	GA		1182

(2) INFORMATION FOR SEQ ID NO:93:

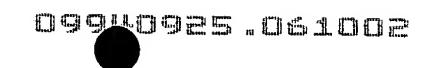
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1182 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double

 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:93:

ATGGAGGAGC	CGCAGTCAGA	TCCTAGCGTC	GAGCCCCCTC	TGAGTCAGGA	AACATTTTCA	60
GACCTATGGA	AACTACTTCC	TGAAAACAAC	GTTCTGTCCC	CCTTGCCGTC	CCAAGCAATG	120
GATGATTTGA	TGCTGTCCCC	GGACGATATT	GAACAATGGT	TCACTGAAGA	CCCAGGTCCA	180
GATGAAGCTC	CCAGAATGCC	AGAGGCTGCT	CCCCCGTGG	CCCCTGCACC	AGCAGCTCCT	240
ACACCGGCGG	CCCCTGCACC	AGCCCCCTCC	TGGCCCCTGT	CATCTTCTGT	CCCTTCCCAG	300
AAAACCTACC	AGGGCAGCTA	CGGTTTCCGT	CTGGGCTTCT	TGCATTCTGG	GACAGCCAAG	360
TCTGTGACTT	GCACGTACTC	CCCTGCCCTC	AACAAGATGT	TTTGCCAACT	GGCCAAGACC	420
TGCCCTGCGC	AGCTGTGGGT	TGATTCCACA	CCCCCGCCCG	GCACCCGCGT	CCGCGCCATG	480
GCCATCTACA	AGCAGTCACA	GCACATGACG	GAGGTTGTGA	GGCGCTGCCC	CCACCATGAG	540
CGCTGCTCAG	ATAGCGATGG	TCTGGCCCCT	CCTCAGCATC	TTATCCGAGT	GGAAGGAAAT	600
TTGCGTGTGG	AGTATTTGGA	TGACAGAAAC	ACTTTTCGAC	ATAGTGTGGT	GGTGCCCTAT	660
GAGCCGCCTG	AGGTTGGCTC	TGACTGTACC	ACCATCCACT	ACAACTACAT	GTGTAACAGT	720
TCCTGCATGG	GCGGCATGAA	CCGGAGGCCC	ATCCTCACCA	TCATCACACT	GGAAGACTCC	780
AGTGGTAATC	TACTGGGACG	GAACAGCTTT	GAGGTGCGTG	TTTGTGCCTG	TCCTGGGAGA	840
GACCGGCGCA	CAGAGGAAGA	GAATCTCCGC	AAGAAAGGGG	AGCCTCACCA	CGAGCTGCCC	900



CCAGGGAGCA	CTAAGCGAGC	ACTGCCCAAC	AACACCAGCT	CCTCTCCCCA	GCCAAAGAAG	960
AAACCACTGG	ATGGAGAATA	TTTCACCCTT	CAGATCCGTG	GGCGTGAGCG	CTTCGAGATG	1020
TTCCGAGAGC	TGAATGAGGC	CTTGGAACTC	AAGGATGCCC	AGGCTGGGAA	GGAGCCAGGG	1080
GGGAGCAGGG	CTCACTCCAG	CCACCTGAAG	TCCAAAAAGG	GTCAGTCTAC	CTCCCGCCAT	1140
AAAAAACTCA	TGTTCAAGAC	AGAAGGGCCT	GACTCAGACT	GA		1182

(2) INFORMATION FOR SEQ ID NO:94:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1182 base pairs (B) TYPE: nucleic acid

 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:94:

ATGGAGGAGC	CGCAGTCAGA	TCCTAGCGTC	GAGCCCCCTC	TGAGTCAGGA	AACATTTTCA	60
GACCTATGGA	AACTACTTCC	TGAAAACAAC	GTTCTGTCCC	CCTTGCCGTC	CCAAGCAATG	120
GATGATTTGA	TGCTGTCCCC	GGACGATATT	GAACAATGGT	TCACTGAAGA	CCCAGGTCCA	180
GATGAAGCTC	CCAGAATGCC	AGAGGCTGCT	CCCCCGTGG	CCCCTGCACC	AGCAGCTCCT	240
ACACCGGCGG	CCCCTGCACC	AGCCCCCTCC	TGGCCCCTGT	CATCTTCTGT	CCCTTCCCAG	300
AAAACCTACC	AGGGCAGCTA	CGGTTTCCGT	CTGGGCTTCT	TGCATTCTGG	GACAGCCAAG	360
TCTGTGACTT	GCACGTACTC	CCCTGCCCTC	AACAAGATGT	TTTGCCAACT	GGCCAAGACC	420
TGCCCTGTGC	AGCTGTGGGT	TGATTCCACA	CCCCCGCCCG	GCACCCGCGT	CCGCGCCATG	480
GCCATCTACA	AGCAGTCACA	GCACATGACG	GAGGTTGTGA	GGCGCTGCCC	CCACCATGAG	540
CGCTGCTCAG	ATAGCGATGG	TCTGGCCCCT	CCTCAGCATC	TTATCCGAGT	GGAAGGAAAT	600
TTGCGTGTGG	AGTATTTGGA	TGACAGAAAC	ACTTTTCGAC	ATAGTGTGGT	GGTGCCCTAT	660
GAGCCGCCTG	AGGTTGGCTC	TGACTGTACC	ACCATCCACT	ACAACTACAT	GTGTAACAGT	720
TCCTGCATGG	GCGGCATGAA	CCGGAGACCC	ATCCTCACCA	TCATCACACT	GGAAGACTCC	780
AGTGGTAATC	TACTGGGACG	GAACAGCTTT	GAGGTGCGTG	TTTGTGCCTG	TCCTGGGAGA	840
GACCGGCGCA	CAGAGGAAGA	GAATCTCCGC	AAGAAAGGGG	AGCCTCACCA	CGAGCTGCCC	900
CCAGGGAGCA	CTAAGCGAGC	ACTGCCCAAC	AACACCAGCT	CCTCTCCCCA	GCCAAAGAAG	960
AAACCACTGG	ATGGAGAATA	TTTCACCCTT	CAGATCCGTG	GGCGTGAGCG	CTTCGAGATG	1020
TTCCGAGAGC	TGAATGAGGC	CTTGGAACTC	AAGGATGCCC	AGGCTGGGAA	GGAGCCAGGG	1080
GGGAGCAGGG	CTCACTCCAG	CCACCTGAAG	TCCAAAAAGG	GTCAGTCTAC	CTCCCGCCAT	1140
AAAAAACTCA	TGTTCAAGAC	AGAAGGGCCT	GACTCAGACT	GA		1182

OGGLOGE OSLOGE

 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 20 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
(ii) MOLECULE TYPE: DNA (genomic)	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:95:	
TCTGGGCTTC TTGCATTCTG	20
(2) INFORMATION FOR SEQ ID NO:96:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 20 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
(ii) MOLECULE TYPE: DNA (genomic)	
(xi) SEQUENCE DESCRIPTION; SEQ ID NO:96:	
GTTGGGCAGT GCTCGCTTAG	20
(2) INFORMATION FOR SEQ ID NO:97:	
(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 601 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: DNA (genomic)	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:97:	
TCTGGGCTTC TTGCATTCTG GGACAGCCAA GTCTGTGACT TGCACGTACT CCCCTGCCCT	60
CAACAAGATG TTTTGCCAAC TGGCCAAGAC CTGCCCTGTG CAGCTGTGGG TTGATTCCAC	120
ACCCCGCCC GGCACCCGCG TCCGCGCCAT GGCCATCTAC AAGCAGTCAC AGCACATGAC	180
GGAGGTTGTG AGGCGCTGCC CCCACCATGA GCGCTGCTCA GATAGCGATG GTCTGGCCCC	240
TCCTCAGCAT CTTATCCGAG TGGAAGGAAA TTTGCGTGTG GAGTATTTGG ATGACAGAAA	300
CACTTTTCGA CATAGTGTGG TGGTGCCCTA TGAGCCGCCT GAGGTTGGCT CTGACTGTAC	360
CACCATCCAC TACAACTACA TGTGTAACAG TTCCTGCATG GGCGGCATGA ACCGGAGGCC	420
CATCCTCACC ATCATCACAC TGGAAGACTC CAGTGGTAAT CTACTGGGAC GGAACAGCTT	480
TGAGGTGCGT GTTTGTGCCT GTCCTGGGAG AGACCGGCGC ACAGAGGAAG AGAATCTCCG	540
CAAGAAAGGG GAGCCTCACC ACGAGCTGCC CCCAGGGAGC ACTAAGCGAG CACTGCCCAA	600
C	601

(2) INFORMATION FOR SEQ ID NO:95:

(2) INFORMATION FOR SEQ ID NO:98:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 601 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:98:

GTTGGGCAGT	GCTCGCTTAG	TGCTCCCTGG	GGGCAGCTCG	TGGTGAGGCT	CCCCTTTCTT	60
GCGGAGATTC	TCTTCCTCTG	TGCGCCGGTC	TCTCCCAGGA	CAGGCACAAA	CACGCACCTC	120
AAAGCTGTTC	CGTCCCAGTA	GATTACCACT	GGAGTCTTCC	AGTGTGATGA	TGGTGAGGAT	180
GGGCCTCCGG	TTCATGCCGC	CCATGCAGGA	ACTGTTACAC	ATGTAGTTGT	AGTGGATGGT	240
GGTACAGTCA	GAGCCAACCT	CAGGCGGCTC	ATAGGGCACC	ACCACACTAT	GTCGAAAAGT	300
GTTTCTGTCA	TCCAAATACT	CCACACGCAA	ATTTCCTTCC	ACTCGGATAA	GATGCTGAGG	360
AGGGGCCAGA	CCATCGCTAT	CTGAGCAGCG	CTCATGGTGG	GGGCAGCGCC	TCACAACCTC	420
CGTCATGTGC	TGTGACTGCT	TGTAGATGGC	CATGGCGCGG	ACGCGGGTGC	CGGGCGGGG	480
TGTGGAATCA	ACCCACAGCT	GCACAGGGCA	GGTCTTGGCC	AGTTGGCAAA	ACATCTTGTT	540
GAGGGCAGGG	GAGTACGTGC	AAGTCACAGA	CTTGGCTGTC	CCAGAATGCA	AGAAGCCCAG	600
A						601

(2) INFORMATION FOR SEQ ID NO:99:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 601 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:99:

TCTGGGCTTC	TTGCATTCTG	GGACAGCCAA	GTCTGTGACT	TGCACGTACT	CCCCTGCCCT	60
CAACAAGATG	TTTTGCCAAC	TGGCCAAGAC	CTGCCCTGCG	CAGCTGTGGG	TTGATTCCAC	120
ACCCCCGCCC	GGCACCCGCG	TCCGCGCCAT	GGCCATCTAC	AAGCAGTCAC	AGCACATGAC	180
GGAGGTTGTG	AGGCGCTGCC	CCCACCATGA	GCGCTGCTCA	GATAGCGATG	GTCTGGCCCC	240
TCCTCAGCAT	CTTATCCGAG	TGGAAGGAAA	TTTGCGTGTG	GAGTATTTGG	ATGACAGAAA	300
CACTTTTCGA	CATAGTGTGG	TGGTGCCCTA	TGAGCCGCCT	GAGGTTGGCT	CTGACTGTAC	360
CACCATCCAC	TACAACTACA	TGTGTAACAG	TTCCTGCATG	GGCGGCATGA	ACCGGAGGCC	420
CATCCTCACC	ATCATCACAC	TGGAAGACTC	CAGTGGTAAT	CTACTGGGAC	GGAACAGCTT	480

540

CAAGAAAGGG GAGCCTCACC ACGAGCTGCC CCCAGGGAGC ACTAAGCGAG CACTGCCCAA	600					
С	601					
(2) INFORMATION FOR SEQ ID NO:100:						
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 601 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 						
(ii) MOLECULE TYPE: DNA (genomic)						
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:100:						
GTTGGGCAGT GCTCGCTTAG TGCTCCCTGG GGGCAGCTCG TGGTGAGGCT CCCCTTTCTT	60					
GCGGAGATTC TCTTCCTCTG TGCGCCGGTC TCTCCCAGGA CAGGCACAAA CACGCACCTC	120					
AAAGCTGTTC CGTCCCAGTA GATTACCACT GGAGTCTTCC AGTGTGATGA TGGTGAGGAT	180					
GGGCCTCCGG TTCATGCCGC CCATGCAGGA ACTGTTACAC ATGTAGTTGT AGTGGATGGT	240					
GGTACAGTCA GAGCCAACCT CAGGCGGCTC ATAGGGCACC ACCACACTAT GTCGAAAAGT	300					
GTTTCTGTCA TCCAAATACT CCACACGCAA ATTTCCTTCC ACTCGGATAA GATGCTGAGG	360					
AGGGGCCAGA CCATCGCTAT CTGAGCAGCG CTCATGGTGG GGGCAGCGCC TCACAACCTC	420					
CGTCATGTGC TGTGACTGCT TGTAGATGGC CATGGCGCGG ACGCGGGTGC CGGGCGGGG	480					
TGTGGAATCA ACCCACAGCT GCGCAGGGCA GGTCTTGGCC AGTTGGCAAA ACATCTTGTT	540					
GAGGGCAGGG GAGTACGTGC AAGTCACAGA CTTGGCTGTC CCAGAATGCA AGAAGCCCAG	600					
A	601					
(2) INFORMATION FOR SEQ ID NO:101:						
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 601 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 						
(ii) MOLECULE TYPE: DNA (genomic)						
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:101:						
TCTGGGCTTC TTGCATTCTG GGACAGCCAA GTCTGTGACT TGCACGTACT CCCCTGCCCT	60					
CAACAAGATG TTTTGCCAAC TGGCCAAGAC CTGCCCTGTG CAGCTGTGGG TTGATTCCAC	120					
ACCCCCGCCC GGCACCCGCG TCCGCGCCAT GGCCATCTAC AAGCAGTCAC AGCACATGAC	180					
GGAGGTTGTG AGGCGCTGCC CCCACCATGA GCGCTGCTCA GATAGCGATG GTCTGGCCCC	240					
TCCTCAGCAT CTTATCCGAG TGGAAGGAAA TTTGCGTGTG GAGTATTTGG ATGACAGAAA	300					

TGAGGTGCGT GTTTGTGCCT GTCCTGGGAG AGACCGGCGC ACAGAGGAAG AGAATCTCCG

CACTTTTCGA	CATAGTGTGG	TGGTGCCCTA	TGAGCCGCCT	GAGGTTGGCT	CTGACTGTAC	360
CACCATCCAC	TACAACTACA	TGTGTAACAG	TTCCTGCATG	GGCGGCATGA	ACCGGAGACC	420
CATCCTCACC	ATCATCACAC	TGGAAGACTC	CAGTGGTAAT	CTACTGGGAC	GGAACAGCTT	480
TGAGGTGCGT	GTTTGTGCCT	GTCCTGGGAG	AGACCGGCGC	ACAGAGGAAG	AGAATCTCCG	540
CAAGAAAGGG	GAGCCTCACC	ACGAGCTGCC	CCCAGGGAGC	ACTAAGCGAG	CACTGCCCAA	600
С						601
(2) INFORMATION FOR SEQ ID NO:102:						
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 601 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 						

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:102: GTTGGGCAGT GCTCGCTTAG TGCTCCCTGG GGGCAGCTCG TGGTGAGGCT CCCCTTTCTT 60 GCGGAGATTC TCTTCCTCTG TGCGCCGGTC TCTCCCAGGA CAGGCACAAA CACGCACCTC 120 AAAGCTGTTC CGTCCCAGTA GATTACCACT GGAGTCTTCC AGTGTGATGA TGGTGAGGAT 180 GGGTCTCCGG TTCATGCCGC CCATGCAGGA ACTGTTACAC ATGTAGTTGT AGTGGATGGT 240 GGTACAGTCA GAGCCAACCT CAGGCGGCTC ATAGGGCACC ACCACACTAT GTCGAAAAGT 300 GTTTCTGTCA TCCAAATACT CCACACGCAA ATTTCCTTCC ACTCGGATAA GATGCTGAGG 360 AGGGGCCAGA CCATCGCTAT CTGAGCAGCG CTCATGGTGG GGGCAGCGCC TCACAACCTC 420 CGTCATGTGC TGTGACTGCT TGTAGATGGC CATGGCGCGG ACGCGGGTGC CGGGCGGGGG 480 TGTGGAATCA ACCCACAGCT GCACAGGGCA GGTCTTGGCC AGTTGGCAAA ACATCTTGTT 540 GAGGGCAGGG GAGTACGTGC AAGTCACAGA CTTGGCTGTC CCAGAATGCA AGAAGCCCAG 600

(2) INFORMATION FOR SEQ ID NO:103:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:103:

GAGGATGGGA CTCCGGTTCA TG

Α

22

601

(2) INFORMATION FOR SEQ ID NO:104:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 24 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
(ii) MOLECULE TYPE: DNA (genomic)	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:104:	
CATGAACCGG AGTCCCATCC TCAC	24
(2) INFORMATION FOR SEQ ID NO:105:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 23 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
(ii) MOLECULE TYPE: DNA (genomic)	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:105:	
GCACAAACAT GCACCTCAAA GCT	23
(2) INFORMATION FOR SEQ ID NO:106:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 22 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
(ii) MOLECULE TYPE: DNA (genomic)	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:106:	
CAGCTTTGAG GTGCATGTTT GT	22
(2) INFORMATION FOR SEQ ID NO:107:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 601 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
(ii) MOLECULE TYPE: DNA (genomic)	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:107:	
TCTGGGCTTC TTGCATTCTG GGACAGCCAA GTCTGTGACT TGCACGTACT CCCCTGCCCT	60
CAACAAGATG TTTTGCCAAC TGGCCAAGAC CTGCCCTGTG CAGCTGTGGG TTGATTCCAC	120
ACCCCCGCCC GGCACCCGCG TCCGCGCCAT GGCCATCTAC AAGCAGTCAC AGCACATGAC	180
GGAGGTTGTG AGGCGCTGCC CCCACCATGA GCGCTGCTCA GATAGCGATG GTCTGGCCCC	240

TCCTCAGCAT	CTTATCCGAG	TGGAAGGAAA	TTTGCGTGTG	GAGTATTTGG	ATGACAGAAA	300
CACTTTTCGA	CATAGTGTGG	TGGTGCCCTA	TGAGCCGCCT	GAGGTTGGCT	CTGACTGTAC	360
CACCATCCAC	TACAACTACA	TGTGTAACAG	TTCCTGCATG	GGCGGCATGA	ACCGGAGTCC	420
CATCCTCACC	ATCATCACAC	TGGAAGACTC	CAGTGGTAAT	CTACTGGGAC	GGAACAGCTT	480
TGAGGTGCGT	GTTTGTGCCT	GTCCTGGGAG	AGACCGGCGC	ACAGAGGAAG	AGAATCTCCG	540
CAAGAAAGGG	GAGCCTCACC	ACGAGCTGCC	CCCAGGGAGC	ACTAAGCGAG	CACTGCCCAA	600
С						601

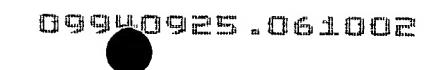
(2) INFORMATION FOR SEQ ID NO:108:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 601 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:108:

GTTGGGCAGT GCTCGCTTAG TGCTCCCTGG GGGCAGCTCG TGGTGAGGCT CCCCTTTCTT 60 GCGGAGATTC TCTTCCTCTG TGCGCCGGTC TCTCCCAGGA CAGGCACAAA CACGCACCTC 120 AAAGCTGTTC CGTCCCAGTA GATTACCACT GGAGTCTTCC AGTGTGATGA TGGTGAGGAT 180 GGGACTCCGG TTCATGCCGC CCATGCAGGA ACTGTTACAC ATGTAGTTGT AGTGGATGGT 240 GGTACAGTCA GAGCCAACCT CAGGCGGCTC ATAGGGCACC ACCACACTAT GTCGAAAAGT 300 GTTTCTGTCA TCCAAATACT CCACACGCAA ATTTCCTTCC ACTCGGATAA GATGCTGAGG 360 AGGGGCCAGA CCATCGCTAT CTGAGCAGCG CTCATGGTGG GGGCAGCGCC TCACAACCTC 420 CGTCATGTGC TGTGACTGCT TGTAGATGGC CATGGCGCGG ACGCGGGTGC CGGGCGGGG 480 TGTGGAATCA ACCCACAGCT GCACAGGGCA GGTCTTGGCC AGTTGGCAAA ACATCTTGTT 540 GAGGGCAGGG GAGTACGTGC AAGTCACAGA CTTGGCTGTC CCAGAATGCA AGAAGCCCAG 600 601 Α

(2) INFORMATION FOR SEQ ID NO:109:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 601 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)



(xi) SEQUENCE DESCRIPTION: SEQ ID NO:109:	
TCTGGGCTTC TTGCATTCTG GGACAGCCAA GTCTGTGACT TGCACGTACT CCCCTGCCCT	60
CAACAAGATG TTTTGCCAAC TGGCCAAGAC CTGCCCTGTG CAGCTGTGGG TTGATTCCAC	120
ACCCCCGCCC GGCACCCGCG TCCGCGCCAT GGCCATCTAC AAGCAGTCAC AGCACATGAC	180
GGAGGTTGTG AGGCGCTGCC CCCACCATGA GCGCTGCTCA GATAGCGATG GTCTGGCCCC	240
TCCTCAGCAT CTTATCCGAG TGGAAGGAAA TTTGCGTGTG GAGTATTTGG ATGACAGAAA	300
CACTTTTCGA CATAGTGTGG TGGTGCCCTA TGAGCCGCCT GAGGTTGGCT CTGACTGTAC	360
CACCATCCAC TACAACTACA TGTGTAACAG TTCCTGCATG GGCGGCATGA ACCGGAGGCC	420
CATCCTCACC ATCATCACAC TGGAAGACTC CAGTGGTAAT CTACTGGGAC GGAACAGCTT	480
TGAGGTGCAT GTTTGTGCCT GTCCTGGGAG AGACCGGCGC ACAGAGGAAG AGAATCTCCG	540
CAAGAAAGGG GAGCCTCACC ACGAGCTGCC CCCAGGGAGC ACTAAGCGAG CACTGCCCAA	600
C	601

(2) INFORMATION FOR SEQ ID NO:110:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 601 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:110:

GTTGGGCAGT GCTCGCTTAG	TGCTCCCTGG	GGGCAGCTCG	TGGTGAGGCT	CCCCTTTCTT	60
GCGGAGATTC TCTTCCTCTG	TGCGCCGGTC	TCTCCCAGGA	CAGGCACAAA	CATGCACCTC	120
AAAGCTGTTC CGTCCCAGTA	GATTACCACT	GGAGTCTTCC	AGTGTGATGA	TGGTGAGGAT	180
GGGCCTCCGG TTCATGCCGC	CCATGCAGGA	ACTGTTACAC	ATGTAGTTGT	AGTGGATGGT	240
GGTACAGTCA GAGCCAACCT	CAGGCGGCTC	ATAGGGCACC	ACCACACTAT	GTCGAAAAGT	300
GTTTCTGTCA TCCAAATACT	CCACACGCAA	ATTTCCTTCC	ACTCGGATAA	GATGCTGAGG	360
AGGGCCAGA CCATCGCTAT	CTGAGCAGCG	CTCATGGTGG	GGGCAGCGCC	TCACAACCTC	420
CGTCATGTGC TGTGACTGCT	TGTAGATGGC	CATGGCGCGG	ACGCGGGTGC	CGGGCGGGG	480
TGTGGAATCA ACCCACAGCT	GCACAGGGCA	GGTCTTGGCC	AGTTGGCAAA	ACATCTTGTT	540
GAGGGCAGGG GAGTACGTGC	AAGTCACAGA	CTTGGCTGTC	CCAGAATGCA	AGAAGCCCAG	600
A					601

(2)	INFORMATION	FOR	SEQ	ID	NO:111:
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- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 427 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:111:

TCTGGGCTTC	TTGCATTCTG	GGACAGCCAA	GTCTGTGACT	TGCACGTACT	CCCCTGCCCT	60
CAACAAGATG	TTTTGCCAAC	TGGCCAAGAC	CTGCCCTGTG	CAGCTGTGGG	TTGATTCCAC	120
ACCCCCGCCC	GGCACCCGCG	TCCGCGCCAT	GGCCATCTAC	AAGCAGTCAC	AGCACATGAC	180
GGAGGTTGTG	AGGCGCTGCC	CCCACCATGA	GCGCTGCTCA	GATAGCGATG	GTCTGGCCCC	240
TCCTCAGCAT	CTTATCCGAG	TGGAAGGAAA	TTTGCGTGTG	GAGTATTTGG	ATGACAGAAA	300
CACTTTTCGA	CATAGTGTGG	TGGTGCCCTA	TGAGCCGCCT	GAGGTTGGCT	CTGACTGTAC	360
CACCATCCAC	TACAACTACA	TGTGTAACAG	TTCCTGCATG	GGCGGCATGA	ACCGGAGTCC	420
CATCCTC						427

(2) INFORMATION FOR SEQ ID NO:112:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 196 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:112:

CATGAACCGG	AGTCCCATCC	TCACCATCAT	CACACTGGAA	GACTCCAGTG	GTAATCTACT	60
GGGACGGAAC	AGCTTTGAGG	TGCGTGTTTG	TGCCTGTCCT	GGGAGAGACC	GGCGCACAGA	120
GGAAGAGAAT	CTCCGCAAGA	AAGGGGAGCC	TCACCACGAG	CTGCCCCCAG	GGAGCACTAA	180
GCGAGCACTG	CCCAAC					196

(2) INFORMATION FOR SEQ ID NO:113:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 498 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:113:	
TCTGGGCTTC TTGCATTCTG GGACAGCCAA GTCTGTGACT TGCACGTACT CCCCTGCCCT	60
CAACAAGATG TTTTGCCAAC TGGCCAAGAC CTGCCCTGTG CAGCTGTGGG TTGATTCCAC	120
ACCCCCCCC GGCACCCGCG TCCGCGCCAT GGCCATCTAC AAGCAGTCAC AGCACATGAC	180
GGAGGTTGTG AGGCGCTGCC CCCACCATGA GCGCTGCTCA GATAGCGATG GTCTGGCCCC	240
TCCTCAGCAT CTTATCCGAG TGGAAGGAAA TTTGCGTGTG GAGTATTTGG ATGACAGAAA	300
CACTTTTCGA CATAGTGTGG TGGTGCCCTA TGAGCCGCCT GAGGTTGGCT CTGACTGTAC	360
CACCATCCAC TACAACTACA TGTGTAACAG TTCCTGCATG GGCGGCATGA ACCGGAGGCC	420
CATCCTCACC ATCATCACAC TGGAAGACTC CAGTGGTAAT CTACTGGGAC GGAACAGCTT	480
TGAGGTGCAT GTTTGTGC	498
(2) INFORMATION FOR SEQ ID NO:114:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 127 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
(ii) MOLECULE TYPE: DNA (genomic)	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:114:	
CAGCTTTGAG GTGCATGTTT GTGCCTGTCC TGGGAGAGAC CGGCGCACAG AGGAAGAGAA	60
TCTCCGCAAG AAAGGGGAGC CTCACCACGA GCTGCCCCCA GGGAGCACTA AGCGAGCACT	120
GCCCAAC	127
(2) INFORMATION FOR SEQ ID NO:115:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 20 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
(ii) MOLECULE TYPE: DNA (genomic)	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:115:	
GGTTTTCTT TGAGGTTTAG	20
(2) INFORMATION FOR SEQ ID NO:116:	
(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 19 base pairs(B) TYPE: nucleic acid	

(ii) MOLECULE TYPE: DNA (genomic)

(D) TOPOLOGY: linear

(C) STRANDEDNESS: single

	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:116:	
GCGA	CACTCC ACCATAGAT	19
(2)	INFORMATION FOR SEQ ID NO:117:	
	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 19 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
	(ii) MOLECULE TYPE: DNA (genomic)	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:117:	
CTGT	CTTCAC GCAGAAAGC	19
(2)	INFORMATION FOR SEQ ID NO:118:	
	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 19 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
	(ii) MOLECULE TYPE: DNA (genomic)	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:118:	
GCAC	GGTCTA CGAGACCTC	19
(2)	INFORMATION FOR SEQ ID NO:119:	
	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 20 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
	(ii) MOLECULE TYPE: DNA (genomic)	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:119:	
GATC	TACTAG TCATATGGAT	20
(2)	INFORMATION FOR SEQ ID NO:120:	
	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 20 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
	(ii) MOLECULE TYPE: DNA (genomic)	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:120:	
TCGG	TACCCG GGGATCCGAT	20

(2) INFORMATION	FOR	SEQ	ΙĎ	NO:121:
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- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 281 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:121:

CTGTCTTCAC GCAGAAAGCG TCTGGCCATG GCGTTAGTAT GAGTGTCGTG CAGCCTCCAG 60

GACCCCCCCT CCCGGGAGAG CCATAGTGGT CTGCGGAACC GGTGAGTACA CCGGAATTGC 120

CAGGACGACC GGGTCCTTTC TTGGATAAAC CCGCTCAATG CCTGGAGATT TGGGCGTGCC 180

CCCGCAAGAC TGCTAGCCGA GTAGTGTTGG GTCGCGAAAG GCCTTGTGGT ACTGCCTGAT 240

AGGGTGCCTG CGAGTGCCCC GGGAGGTCTC GTAGACCGTG C 281

- (2) INFORMATION FOR SEQ ID NO:122:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 386 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:122:

CTGTCTTCAC GCAGAAAGCG TCTGGCCATG GCGTTAGTAT GAGTGTCGTG CAGCCTCCAG 60

GACCCCCCCT CCCGGGAGAG CCATAGTGGT CTGCGGAACC GGTGACTGTC TTCACGCAGA 120

AAGCGTCTAG CCATGGCGTT AGTATGAGTG TCGTGCAGCC TCCAGGACCC CCCCTCCCGG 180

GAGAGCCATA GTGGTCTGCG GAACCGGTGA GTACACCGGA ATTGCCAGGA CGACCGGGTC 240

CTTTCTTGGA TCAACCCGCT CAATGCCTGG AGATTTGGGC GTGCCCCCGC AAGACTGCTA 300

GCCCGGGAG GTCTCGTAGA CCGTGC 386

- (2) INFORMATION FOR SEQ ID NO:123:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 281 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)

281

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:123:	
CTGTCTTCAC GCAGAAAGCG TCTAGCCATG GCGTTAGTAT GAGTGTCGTG CAGCCTCCAG	60
GTCCCCCCT CCCGGGAGAG CCATAGTGGT CTGCGGAACC GGTGAGTACA CCGGAATTGC	120
CAGGACGACC GGGTCCTTTC TTGGATCAAC CCGCTCAATG CCTGGAGATT TGGGCGTGCC	180
CCCGCGAGAC TGCTAGCCGA GTAGTGTTGG GTCGCGAAAG GCCTTGTGGT ACTGCCTGAT	240
AGGGTGCTTG CGAGTGCCCC GGGAGGTCTC GTAGACCGTG C	281
(2) INFORMATION FOR SEQ ID NO:124:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 282 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
(ii) MOLECULE TYPE: DNA (genomic)	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:124:	
CTGTCTTCAC GCAGAAAGCG TCTAGCCATG GCGTTAGTAT GAGTGTCGTG CAGCCTCCAG	60
GACCCCCCT CCCGGGAGAG CCATAGTGGT CTGCGGAACC GGTGAGTACA CCGGAATTGC	120
CAGGACGACC GGGTCCTTTC GTGGATGTAA CCCGCTCAAT GCCTGGAGAT TTGGGCGTGC	180
CCCCGCAAGA CTGCTAGCCG AGTAGTGTTG GGTCGCGAAA GGCCTTGTGG TACTGCCTGA	240
TAGGGTGCTT GCGAGTGCCC CGGGAGGTCT CGTAGACCGT GC	282
(2) INFORMATION FOR SEQ ID NO:125:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 281 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
(ii) MOLECULE TYPE: DNA (genomic)	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:125:	
CTGTCTTCAC GCAGAAAGCG TCTAGCCATG GCGTTAGTAT GAGTGTCGTA CAGCCTCCAG	60
GCCCCCCCT CCCGGGAGAG CCATAGTGGT CTGCGGAACC GGTGAGTACA CCGGAATTGC	120
CGGGAAGACT GGGTCCTTTC TTGGATAAAC CCACTCTATG CCCGGCCATT TGGGCGTGCC	180

CCCGCAAGAC TGCTAGCCGA GTAGCGTTGG GTTGCGAAAG GCCTTGTGGT ACTGCCTGAT

AGGGTGCTTG CGAGTACCCC GGGAGGTCTC GTAGACCGTG C

180

240

281

(2) INFORMATION FOR SEQ ID NO:126:	
(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 281 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: DNA (genomic)	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:126:	
CTGTCTTCAC GCAGAAAGCG CCTAGCCATG GCGTTAGTAC GAGTGTCGTG CAGCCTCCAG	60
GACCCCCCT CCCGGGAGAG CCATAGTGGT CTGCGGAACC GGTGAGTACA CCGGAATCGC	120
TGGGGTGACC GGGTCCTTTC TTGGAGCAAC CCGCTCAATA CCCAGAAATT TGGGCGTGCC	180
CCCGCGAGAT CACTAGCCGA GTAGTGTTGG GTCGCGAAAG GCCTTGTGGT ACTGCCTGAT	240
AGGGTGCTTG CGAGTGCCCC GGGAGGTCTC GTAGACCGTG C	281
(2) INFORMATION FOR SEQ ID NO:127:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 281 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
(ii) MOLECULE TYPE: DNA (genomic)	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:127:	
GCACGGTCTA CGAGACCTCC CGGGGCACTC GCAGGCACCC TATCAGGCAG TACCACAAGG	60

CATACTAACG CCATGGCCAG ACGCTTTCTG CGTGAAGACA G

(2) INFORMATION FOR SEQ ID NO:128:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 281 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)

CCTTTCGCGA CCCAACACTA CTCGGCTAGC AGTCTTGCGG GGGCACGCCC AAATCTCCAG

GCATTGAGCG GGTTTATCCA AGAAAGGACC CGGTCGTCCT GGCAATTCCG GTGTACTCAC

CGGTTCCGCA GACCACTATG GCTCTCCCGG GAGGGGGGGT CCTGGAGGCT GCACGACACT

282

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:128:	
GCACGGTCTA CGAGACCTCC CGGGGCACTC GCAAGCACCC TATCAGGCAG TACCACAAGG	60
CCTTTCGCGA CCCAACACTA CTCGGCTAGC AGTCTTGCGG GGGCACGCCC AAATCTCCAG	120
GCATTGAGCG GGTTGATCCA AGAAAGGACC CGGTCGTCCT GGCAATTCCG GTGTACTCAC	180
CGGTTCCGCA GACCACTATG GCTCTCCCGG GAGGGGGGGT CCTGGAGGCT GCACGACACT	240
CATACTAACG CCATGGCTAG ACGCTTTCTG CGTGAAGACA G	281
(2) INFORMATION FOR SEQ ID NO:129:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 281 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
(ii) MOLECULE TYPE: DNA (genomic)	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:129:	
GCACGGTCTA CGAGACCTCC CGGGGCACTC GCAAGCACCC TATCAGGCAG TACCACAAGG	60
CCTTTCGCGA CCCAACACTA CTCGGCTAGC AGTCTCGCGG GGGCACGCCC AAATCTCCAG	120
GCATTGAGCG GGTTGATCCA AGAAAGGACC CGGTCGTCCT GGCAATTCCG GTGTACTCAC	180
CGGTTCCGCA GACCACTATG GCTCTCCCGG GAGGGGGGGA CCTGGAGGCT GCACGACACT	240
CATACTAACG CCATGGCTAG ACGCTTTCTG CGTGAAGACA G	281
(2) INFORMATION FOR SEQ ID NO:130:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 282 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
(ii) MOLECULE TYPE: DNA (genomic)	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:130:	
GCACGGTCTA CGAGACCTCC CGGGGCACTC GCAAGCACCC TATCAGGCAG TACCACAAGG	60
CCTTTCGCGA CCCAACACTA CTCGGCTAGC AGTCTTGCGG GGGCACGCCC AAATCTCCAG	120
GCATTGAGCG GGTTACATCC ACGAAAGGAC CCGGTCGTCC TGGCAATTCC GGTGTACTCA	180

CCGGTTCCGC AGACCACTAT GGCTCTCCCG GGAGGGGGGG TCCTGGAGGC TGCACGACAC

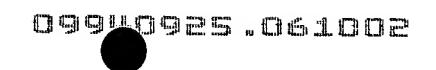
TCATACTAAC GCCATGGCTA GACGCTTTCT GCGTGAAGAC AG

(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 281 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: DNA (genomic)	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:131:	
GCACGGTCTA CGAGACCTCC CGGGGTACTC GCAAGCACCC TATCAGGCAG TACCACAAGG	60
CCTTTCGCAA CCCAACGCTA CTCGGCTAGC AGTCTTGCGG GGGCACGCCC AAATGGCCGG	120
GCATAGAGTG GGTTTATCCA AGAAAGGACC CAGTCTTCCC GGCAATTCCG GTGTACTCAC	180
CGGTTCCGCA GACCACTATG GCTCTCCCGG GAGGGGGGG CCTGGAGGCT GTACGACACT	240
CATACTAACG CCATGGCTAG ACGCTTTCTG CGTGAAGACA G	281
(2) INFORMATION FOR SEQ ID NO:132:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 281 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
(ii) MOLECULE TYPE: DNA (genomic)	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:132:	
GCACGGTCTA CGAGACCTCC CGGGGCACTC GCAAGCACCC TATCAGGCAG TACCACAAGG	60
CCTTTCGCGA CCCAACACTA CTCGGCTAGT GATCTCGCGG GGGCACGCCC AAATTTCTGG	120
GTATTGAGCG GGTTGCTCCA AGAAAGGACC CGGTCACCCC AGCGATTCCG GTGTACTCAC	180
CGGTTCCGCA GACCACTATG GCTCTCCCGG GAGGGGGGT CCTGGAGGCT GCACGACACT	240
CGTACTAACG CCATGGCTAG GCGCTTTCTG CGTGAAGACA G	281
(2) INFORMATION FOR SEQ ID NO:133:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 20 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
(ii) MOLECULE TYPE: DNA (genomic)	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:133:	
ATCAACATCC GGCCGGTGGT	20

(2) INFORMATION FOR SEQ ID NO:131:

 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 20 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
(ii) MOLECULE TYPE: DNA (genomic)	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:134:	
GGGGCCTCGC TACGGACCAG	20
(2) INFORMATION FOR SEQ ID NO:135:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 620 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
(ii) MOLECULE TYPE: DNA (genomic)	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:135:	
ATCAACATCC GGCCGGTGGT CGCCGCGATC AAGGAGTTCT TCGGCACCAG CCAGCTGAGC	60
CAATTCATGG ACCAGAACAA CCCGCTGTCG GGGTTGACCC ACAAGCGCCG ACTGTCGGCG	120
CTGGGGCCCG GCGGTCTGTC ACGTGAGCGT GCCGGGCTGG AGGTCCGCGA CGTGCACCCG	180
TCGCACTACG GCCGGATGTG CCCGATCGAA ACCCCTGAGG GGCCCAACAT CGGTCTGATC	240
GGCTCGCTGT CGGTGTACGC GCGGGTCAAC CCGTTCGGGT TCATCGAAAC GCCGTACCGC	300
AAGGTGGTCG ACGGCGTGGT TAGCGACGAG ATCGTGTACC TGACCGCCGA CGAGGAGGAC	360
CGCCACGTGG TGGCACAGGC CAATTCGCCG ATCGATGCGG ACGGTCGCTT CGTCGAGCCG	420
CGCGTGCTGG TCCGCCGCAA GGCGGGCGAG GTGGAGTACG TGCCCTCGTC TGAGGTGGAC	480
TACATGGACG TCTCGCCCCG CCAGATGGTG TCGGTGGCCA CCGCGATGAT TCCCTTCCTG	540
GAGCACGACG ACGCCAACCG TGCCCTCATG GGGGCAAACA TGCAGCGCCA GGCGGTGCCG	600
CTGGTCCGTA GCGAGGCCCC	620
(2) INFORMATION FOR SEQ ID NO:136:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 620 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
(ii) MOLECULE TYPE: DNA (genomic)	

(2) INFORMATION FOR SEQ ID NO:134:



(xi) SEQUENCE DESCRIPTION: SEQ ID NO:136:

ATCAACATCC GGCCGGTGGT CGCCGCGATC AAGGAGTTCT TCGGCACCAG CCAGCTGAGC 60 CAATTCATGG ACCAGAACAA CCCGCTGTCG GGGTTGACCT ACAAGCGCCG ACTGTCGGCG 120 CTGGGGCCCG GCGGTCTGTC ACGTGAGCGT GCCGGGCTGG AGGTCCGCGA CGTGCACCCG 180 TCGCACTACG GCCGGATGTG CCCGATCGAA ACCCCTGAGG GGCCCAACAT CGGTCTGATC 240 GGCTCGCTGT CGGTGTACGC GCGGGTCAAC CCGTTCGGGT TCATCGAAAC GCCGTACCGC 300 AAGGTGGTCG ACGGCGTGGT TAGCGACGAG ATCGTGTACC TGACCGCCGA CGAGGAGGAC 360 CGCCACGTGG TGGCACAGGC CAATTCGCCG ATCGATGCGG ACGGTCGCTT CGTCGAGCCG 420 CGCGTGCTGG TCCGCCGCAA GGCGGGCGAG GTGGAGTACG TGCCCTCGTC TGAGGTGGAC 480 TACATGGACG TCTCGCCCCG CCAGATGGTG TCGGTGGCCA CCGCGATGAT TCCCTTCCTG 540 GAGCACGACG ACGCCAACCG TGCCCTCATG GGGGCAAACA TGCAGCGCCA GGCGGTGCCG 600 CTGGTCCGTA GCGAGGCCCC 620

(2) INFORMATION FOR SEQ ID NO:137:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 620 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:137:

ATCAACATCC GGCCGGTGGT CGCCGCGATC AAGGAGTTCT TCGGCACCAG CCAGCTGAGC 60 CAATTCATGG ACCAGAACAA CCCGCTGTCG GGGTTGACCC ACAAGCGCCG ACTGTTGGCG 120 CTGGGGCCCG GCGGTCTGTC ACGTGAGCGT GCCGGGCTGG AGGTCCGCGA CGTGCACCCG 180 TCGCACTACG GCCGGATGTG CCCGATCGAA ACCCCTGAGG GGCCCAACAT CGGTCTGATC 240 GGCTCGCTGT CGGTGTACGC GCGGGTCAAC CCGTTCGGGT TCATCGAAAC GCCGTACCGC 300 AAGGTGGTCG ACGGCGTGGT TAGCGACGAG ATCGTGTACC TGACCGCCGA CGAGGAGGAC 360 CGCCACGTGG TGGCACAGGC CAATTCGCCG ATCGATGCGG ACGGTCGCTT CGTCGAGCCG 420 CGCGTGCTGG TCCGCCGCAA GGCGGGCGAG GTGGAGTACG TGCCCTCGTC TGAGGTGGAC 480 TACATGGACG TCTCGCCCCG CCAGATGGTG TCGGTGGCCA CCGCGATGAT TCCCTTCCTG 540 GAGCACGACG ACGCCAACCG TGCCCTCATG GGGGCAAACA TGCAGCGCCA GGCGGTGCCG 600 CTGGTCCGTA GCGAGGCCCC 620

(2) INFORMATION FOR SEQ ID NO:138:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 620 base pairs

 - (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:138:

GGGGCCTCGC	TACGGACCAG	CGGCACCGCC	TGGCGCTGCA	TGTTTGCCCC	CATGAGGGCA	60
CGGTTGGCGT	CGTCGTGCTC	CAGGAAGGGA	ATCATCGCGG	TGGCCACCGA	CACCATCTGG	120
CGGGGCGAGA	CGTCCATGTA	GTCCACCTCA	GACGAGGGCA	CGTACTCCAC	CTCGCCCGCC	180
TTGCGGCGGA	CCAGCACGCG	CGGCTCGACG	AAGCGACCGT	CCGCATCGAT	CGGCGAATTG	240
GCCTGTGCCA	CCACGTGGCG	GTCCTCCTCG	TCGGCGGTCA	GGTACACGAT	CTCGTCGCTA	300
ACCACGCCGT	CGACCACCTT	GCGGTACGGC	GTTTCGATGA	ACCCGAACGG	GTTGACCCGC	360
GCGTACACCG	ACAGCGAGCC	GATCAGACCG	ATGTTGGGCC	CCTCAGGGGT	TTCGATCGGG	420
CACATCCGGC	CGTAGTGCGA	CGGGTGCACG	TCGCGGACCT	CCAGCCCGGC	ACGCTCACGT	480
GACAGACCGC	CGGGCCCCAG	CGCCGACAGT	CGGCGCTTGT	GGGTCAACCC	CGACAGCGGG	540
TTGTTCTGGT	CCATGAATTG	GCTCAGCTGG	CTGGTGCCGA	AGAACTCCTT	GATCGCGGCG	600
ACCACCGGCC	GGATGTTGAT					620

(2) INFORMATION FOR SEQ ID NO:139:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 620 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:139:

GGGGCCTCGC	TACGGACCAG	CGGCACCGCC	TGGCGCTGCA	TGTTTGCCCC	CATGAGGGCA	60
CGGTTGGCGT	CGTCGTGCTC	CAGGAAGGGA	ATCATCGCGG	TGGCCACCGA	CACCATCTGG	120
CGGGGCGAGA	CGTCCATGTA	GTCCACCTCA	GACGAGGGCA	CGTACTCCAC	CTCGCCCGCC	180
TTGCGGCGGA	CCAGCACGCG	CGGCTCGACG	AAGCGACCGT	CCGCATCGAT	CGGCGAATTG	240
GCCTGTGCCA	CCACGTGGCG	GTCCTCCTCG	TCGGCGGTCA	GGTACACGAT	CTCGTCGCTA	300
ACCACGCCGT	CGACCACCTT	GCGGTACGGC	GTTTCGATGA	ACCCGAACGG	GTTGACCCGC	360
GCGTACACCG	ACAGCGAGCC	GATCAGACCG	ATGTTGGGCC	CCTCAGGGGT	TTCGATCGGG	420
CACATCCGGC	CGTAGTGCGA	CGGGTGCACG	TCGCGGACCT	CCAGCCCGGC	ACGCTCACGT	480

GACAGACCGC CGGGCCCCAG CGCCGACAGT CGGCGCTTGT AGGTCAACCC CGACAGCGGG	540
TTGTTCTGGT CCATGAATTG GCTCAGCTGG CTGGTGCCGA AGAACTCCTT GATCGCGGCG	600
ACCACCGGCC GGATGTTGAT	620
(2) INFORMATION FOR SEQ ID NO:140:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 620 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
(ii) MOLECULE TYPE: DNA (genomic)	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:140:	
GGGGCCTCGC TACGGACCAG CGGCACCGCC TGGCGCTGCA TGTTTGCCCC CATGAGGGCA	60
CGGTTGGCGT CGTCGTGCTC CAGGAAGGGA ATCATCGCGG TGGCCACCGA CACCATCTGG	120
CGGGGCGAGA CGTCCATGTA GTCCACCTCA GACGAGGGCA CGTACTCCAC CTCGCCCGCC	180
TTGCGGCGGA CCAGCACGCG CGGCTCGACG AAGCGACCGT CCGCATCGAT CGGCGAATTG	240
GCCTGTGCCA CCACGTGGCG GTCCTCCTCG TCGGCGGTCA GGTACACGAT CTCGTCGCTA	300
ACCACGCCGT CGACCACCTT GCGGTACGGC GTTTCGATGA ACCCGAACGG GTTGACCCGC	360
GCGTACACCG ACAGCGAGCC GATCAGACCG ATGTTGGGCC CCTCAGGGGT TTCGATCGGG	420
CACATCCGGC CGTAGTGCGA CGGGTGCACG TCGCGGACCT CCAGCCCGGC ACGCTCACGT	480
GACAGACCGC CGGGCCCCAG CGCCAACAGT CGGCGCTTGT GGGTCAACCC CGACAGCGGG	540
TTGTTCTGGT CCATGAATTG GCTCAGCTGG CTGGTGCCGA AGAACTCCTT GATCGCGGCG	600
ACCACCGGCC GGATGTTGAT	620
(2) INFORMATION FOR SEQ ID NO:141:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 20 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
(ii) MOLECULE TYPE: DNA (genomic)	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:141:	
AGCTCGTATG GCACCGGAAC	20
(2) INFORMATION FOR SEQ ID NO:142:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 20 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	

(ii) MOLECULE TYPE: DNA (genomic)	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:142:	
TTGACCTCCC ACCCGACTTG	20
(2) INFORMATION FOR SEQ ID NO:143:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 620 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
(ii) MOLECULE TYPE: DNA (genomic)	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:143:	
AGCTCGTATG GCACCGGAAC CGGTAAGGAC GCGATCACCA GCGGCATCGA GGTCGTATGG	60
ACGAACACCC CGACGAAATG GGACAACAGT TTCCTCGAGA TCCTGTACGG CTACGAGTGG	120
GAGCTGACGA AGAGCCCTGC TGGCGCTTGG CAATACACCG CCAAGGACGG CGCCGGTGCC	180
GGCACCATCC CGGACCCGTT CGGCGGCCCA GGGCGCTCCC CGACGATGCT GGCCACTGAC	240
CTCTCGCTGC GGGTGGATCC GATCTATGAG CGGATCACGC GTCGCTGGCT GGAACACCCC	300
GAGGAATTGG CCGACGAGTT CGCCAAGGCC TGGTACAAGC TGATCCACCG AGACATGGGT	360
CCCGTTGCGA GATACCTTGG GCCGCTGGTC CCCAAGCAGA CCCTGCTGTG GCAGGATCCG	420
GTCCCTGCGG TCAGCCACGA CCTCGTCGGC GAAGCCGAGA TTGCCAGCCT TAAGAGCCAG	480
ATCCGGGCAT CGGGATTGAC TGTCTCACAG CTAGTTTCGA CCGCATGGGC GGCGGCGTCG	540
TCGTTCCGTG GTAGCGACAA GCGCGGCGGC GCCAACGGTG GTCGCATCCG CCTGCAGCCA	600
CAAGTCGGGT GGGAGGTCAA	620
(2) INFORMATION FOR SEQ ID NO:144:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 620 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
(ii) MOLECULE TYPE: DNA (genomic)	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:144:	
AGCTCGTATG GCACCGGAAC CGGTAAGGAC GCGATCACCA CCGGCATCGA GGTCGTATGG	60
ACGAACACCC CGACGAAATG GGACAACAGT TTCCTCGAGA TCCTGTACGG CTACGAGTGG	120
GAGCTGACGA AGAGCCCTGC TGGCGCTTGG CAATACACCG CCAAGGACGG CGCCGGTGCC	180
GGCACCATCC CGGACCCGTT CGGCGGGCCA GGGCGCTCCC CGACGATGCT GGCCACTGAC	240

CTCTCGCTGC GGGTGGATCC GATCTATGAG CGGATCACGC GTCGCTGGCT GGAACACCCC

GAGGAATTGG	CCGACGAGTT	CGCCAAGGCC	TGGTACAAGC	TGATCCACCG	AGACATGGGT	360
CCCGTTGCGA	GATACCTTGG	GCCGCTGGTC	CCCAAGCAGA	CCCTGCTGTG	GCAGGATCCG	420
GTCCCTGCGG	TCAGCCACGA	CCTCGTCGGC	GAAGCCGAGA	TTGCCAGCCT	TAAGAGCCAG	480
ATCCGGGCAT	CGGGATTGAC	TGTCTCACAG	CTAGTTTCGA	CCGCATGGGC	GGCGGCGTCG	540
TCGTTCCGTG	GTAGCGACAA	GCGCGGCGGC	GCCAACGGTG	GTCGCATCCG	CCTGCAGCCA	600
CAAGTCGGGT	GGGAGGTCAA					620

(2) INFORMATION FOR SEQ ID NO:145:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 620 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:145:

60 AGCTCGTATG GCACCGGAAC CGGTAAGGAC GCGATCACCA GCGGCATCGA GGTCGTATGG ACGAACACCC CGACGAAATG GGACAACAGT TTCCTCGAGA TCCTGTACGG CTACGAGTGG 120 GAGCTGACGA AGAGCCCTGC TGGCGCTTGG CAATACACCG CCAAGGACGG CGCCGGTGCC 180 GGCACCATCC CGGACCCGTT CGGCGGGCCA GGGCGCTCCC CGACGATGCT GGCCACTGAC 240 CTCTCGCTGC GGGTGGATCC GATCTATGAG CGGATCACGC GTCGCTGGCT GGAACACCCC 300 GAGGAATTGG CCGACGAGTT CGCCAAGGCC TGGTACAAGC TGATCCACCG AGACATGGGT 360 CCCGTTGCGA GATACCTTGG GCCGCTGGTC CCCAAGCAGA CCCTGCTGTG GCAGGATCCG 420 GTCCCTGCGG TCAGCCACGA CCTCGTCGGC GAAGCCGAGA TTGCCAGCCT TAAGAGCCAG 480 ATCCTGGCAT CGGGATTGAC TGTCTCACAG CTAGTTTCGA CCGCATGGGC GGCGGCGTCG 540 600 TCGTTCCGTG GTAGCGACAA GCGCGGCGGC GCCAACGGTG GTCGCATCCG CCTGCAGCCA 620 CAAGTCGGGT GGGAGGTCAA

(2) INFORMATION FOR SEQ ID NO:146:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 620 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:146:

AGCTCGTATG GCACCGGAAC CGGTAAGGAC GCGATCACCA CCGGCATCGA GGTCGTATGG 60 ACGAACACCC CGACGAAATG GGACAACAGT TTCCTCGAGA TCCTGTACGG CTACGAGTGG 120 GAGCTGACGA AGAGCCCTGC TGGCGCTTGG CAATACACCG CCAAGGACGG CGCCGGTGCC 180 GGCACCATCC CGGACCCGTT CGGCGGCCCA GGGCGCTCCC CGACGATGCT GGCCACTGAC 240 CTCTCGCTGC GGGTGGATCC GATCTATGAG CGGATCACGC GTCGCTGGCT GGAACACCCC 300 GAGGAATTGG CCGACGAGTT CGCCAAGGCC TGGTACAAGC TGATCCACCG AGACATGGGT 360 CCCGTTGCGA GATACCTTGG GCCGCTGGTC CCCAAGCAGA CCCTGCTGTG GCAGGATCCG 420 GTCCCTGCGG TCAGCCACGA CCTCGTCGGC GAAGCCGAGA TTGCCAGCCT TAAGAGCCAG 480 ATCCTGGCAT CGGGATTGAC TGTCTCACAG CTAGTTTCGA CCGCATGGGC GGCGGCGTCG 540 TCGTTCCGTG GTAGCGACAA GCGCGGCGGC GCCAACGGTG GTCGCATCCG CCTGCAGCCA 600 CAAGTCGGGT GGGAGGTCAA 620

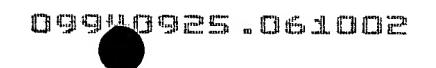
(2) INFORMATION FOR SEQ ID NO:147:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 620 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:147:

TTGACCTCCC ACCCGACTTG TGGCTGCAGG CGGATGCGAC CACCGTTGGC GCCGCCGCGC 60 TTGTCGCTAC CACGGAACGA CGACGCCGCC GCCCATGCGG TCGAAACTAG CTGTGAGACA 120 GTCAATCCCG ATGCCCGGAT CTGGCTCTTA AGGCTGGCAA TCTCGGCTTC GCCGACGAGG 180 TCGTGGCTGA CCGCAGGGAC CGGATCCTGC CACAGCAGGG TCTGCTTGGG GACCAGCGGC 240 CCAAGGTATC TCGCAACGGG ACCCATGTCT CGGTGGATCA GCTTGTACCA GGCCTTGGCG 300 AACTCGTCGG CCAATTCCTC GGGGTGTTCC AGCCAGCGAC GCGTGATCCG CTCATAGATC 360 GGATCCACCC GCAGCGAGAG GTCAGTGGCC AGCATCGTCG GGGAGCGCCC TGGCCCGCCG 420 AACGGGTCCG GGATGGTGCC GGCACCGGCG CCGTCCTTGG CGGTGTATTG CCAAGCGCCA 480 GCAGGGCTCT TCGTCAGCTC CCACTCGTAG CCGTACAGGA TCTCGAGGAA ACTGTTGTCC 540 CATTTCGTCG GGGTGTTCGT CCATACGACC TCGATGCCGC TGGTGATCGC GTCCTTACCG 600 620 GTTCCGGTGC CATACGAGCT



(2) INFORMATION FOR SEQ ID NO:148:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 620 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:148:

TTGACCTCCC	ACCCGACTTG	TGGCTGCAGG	CGGATGCGAC	CACCGTTGGC	GCCGCCGCGC	60
TTGTCGCTAC	CACGGAACGA	CGACGCCGCC	GCCCATGCGG	TCGAAACTAG	CTGTGAGACA	120
GTCAATCCCG	ATGCCCGGAT	CTGGCTCTTA	AGGCTGGCAA	TCTCGGCTTC	GCCGACGAGG	180
TCGTGGCTGA	CCGCAGGGAC	CGGATCCTGC	CACAGCAGGG	TCTGCTTGGG	GACCAGCGGC	240
CCAAGGTATC	TCGCAACGGG	ACCCATGTCT	CGGTGGATCA	GCTTGTACCA	GGCCTTGGCG	300
AACTCGTCGG	CCAATTCCTC	GGGGTGTTCC	AGCCAGCGAC	GCGTGATCCG	CTCATAGATC	360
GGATCCACCC	GCAGCGAGAG	GTCAGTGGCC	AGCATCGTCG	GGGAGCGCCC	TGGCCCGCCG	420
AACGGGTCCG	GGATGGTGCC	GGCACCGGCG	CCGTCCTTGG	CGGTGTATTG	CCAAGCGCCA	480
GCAGGGCTCT	TCGTCAGCTC	CCACTCGTAG	CCGTACAGGA	TCTCGAGGAA	ACTGTTGTCC	540
CATTTCGTCG	GGGTGTTCGT	CCATACGACC	TCGATGCCGG	TGGTGATCGC	GTCCTTACCG	600
GTTCCGGTGC	CATACGAGCT					620

(2) INFORMATION FOR SEQ ID NO:149:

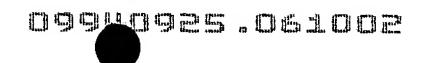
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 620 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:149:

60	GCCGCCGCGC	CACCGTTGGC	CGGATGCGAC	TGGCTGCAGG	ACCCGACTTG	TTGACCTCCC
120	CTGTGAGACA	TCGAAACTAG	GCCCATGCGG	CGACGCCGCC	CACGGAACGA	TTGTCGCTAC
180	GCCGACGAGG	TCTCGGCTTC	AGGCTGGCAA	CTGGCTCTTA	ATGCCAGGAT	GTCAATCCCG
240	GACCAGCGGC	TCTGCTTGGG	CACAGCAGGG	CGGATCCTGC	CCGCAGGGAC	TCGTGGCTGA
300	GGCCTTGGCG	GCTTGTACCA	CGGTGGATCA	ACCCATGTCT	TCGCAACGGG	CCAAGGTATC
360	CTCATAGATC	GCGTGATCCG	AGCCAGCGAC	GGGGTGTTCC	CCAATTCCTC	AACTCGTCGG
420	TGGCCCGCCG	GGGAGCGCCC	AGCATCGTCG	GTCAGTGGCC	GCAGCGAGAG	GGATCCACCC
480	CCAAGCGCCA	CGGTGTATTG	CCGTCCTTGG	GGCACCGGCG	GGATGGTGCC	AACGGGTCCG

GCAGGGCTCT TCGTCAGCTC CCACTCGTAG CCGTACAGGA TCTCGAGGAA ACTGTTGTCC 540
CATTTCGTCG GGGTGTTCGT CCATACGACC TCGATGCCGC TGGTGATCGC GTCCTTACCG 600
GTTCCGGTGC CATACGAGCT (2) INFORMATION FOR SEQ ID NO:150:
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 620 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:150:
TTGACCTCCC ACCCGACTTG TGGCTGCAGG CGGATGCGAC CACCGTTGGC GCCGCCGCGC 60
TTGTCGCTAC CACGGAACGA CGACGCCGCC GCCCATGCGG TCGAAACTAG CTGTGAGACA 120
GTCAATCCCG ATGCCAGGAT CTGGCTCTTA AGGCTGGCAA TCTCGGCTTC GCCGACGAGG 180
TCGTGGCTGA CCGCAGGGAC CGGATCCTGC CACAGCAGGG TCTGCTTGGG GACCAGCGGC 240
CCAAGGTATC TCGCAACGGG ACCCATGTCT CGGTGGATCA GCTTGTACCA GGCCTTGGCG 306
AACTCGTCGG CCAATTCCTC GGGGTGTTCC AGCCAGCGAC GCGTGATCCG CTCATAGATC 360
GGATCCACCC GCAGCGAGAG GTCAGTGGCC AGCATCGTCG GGGAGCGCCC TGGCCCGCCG 420
AACGGGTCCG GGATGGTGCC GGCACCGGCG CCGTCCTTGG CGGTGTATTG CCAAGCGCCA 480
GCAGGGCTCT TCGTCAGCTC CCACTCGTAG CCGTACAGGA TCTCGAGGAA ACTGTTGTCC 540
CATTTCGTCG GGGTGTTCGT CCATACGACC TCGATGCCGG TGGTGATCGC GTCCTTACCG 600
GTTCCGGTGC CATACGAGCT 620
(2) INFORMATION FOR SEQ ID NO:151:
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 20 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:151:
AGAGTTTGAT CCTGGCTCAG
(2) INFORMATION FOR SEQ ID NO:152:
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 17 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear

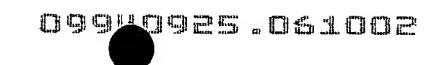
- 90 -

(ii) MOLECULE TYPE: DNA (genomic)	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:152:	
GGCGGACGGG TGAGTAA	17
(2) INFORMATION FOR SEQ ID NO:153:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 20 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
(ii) MOLECULE TYPE: DNA (genomic)	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:153:	
CTGCTGCCTC CCGTAGGAGT	20
(2) INFORMATION FOR SEQ ID NO:154:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 29 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
(ii) MOLECULE TYPE: DNA (genomic)	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:154:	
ATGACGTCAA GTCATCATGG CCCTTACGA	29
(2) INFORMATION FOR SEQ ID NO:155:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 27 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
(ii) MOLECULE TYPE: DNA (genomic)	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:155:	
GTACAAGGCC CGGGAACGTA TTCACCG	27
(2) INFORMATION FOR SEQ ID NO:156:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 16 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
(ii) MOLECULE TYPE: DNA (genomic)	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:156:	
GCAACGAGCG CAACCC	16



(2) INFORMATION FOR SEQ ID NO:157: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 26 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: DNA (genomic) (xi) SEQUENCE DESCRIPTION: SEQ ID NO:157: ATGACGTCAA GTCATCATGG CCCTTA (2) INFORMATION FOR SEQ ID NO:158: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 1542 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (ii) MOLECULE TYPE: DNA (genomic) (xi) SEQUENCE DESCRIPTION: SEQ ID NO:158: AAATTGAAGA GTTTGATCAT GGCTCAGATT GAACGCTGGC GGCAGGCCTA ACACATGCAA

60 GTCGAACGGT AACAGGAAGA AGCTTGCTTC TTTGCTGACG AGTGGCGGAC GGGTGAGTAA 120 180 TGTCTGGGAA ACTGCCTGAT GGAGGGGGAT AACTACTGGA AACGGTAGCT AATACCGCAT AACGTCGCAA GACCAAAGAG GGGGACCTTC GGGCCTCTTG CCATCGGATG TGCCCAGATG 240 GGATTAGCTA GTAGGTGGGG TAACGGCTCA CCTAGGCGAC GATCCCTAGC TGGTCTGAGA 300 360 GGATGACCAG CCACACTGGA ACTGAGACAC GGTCCAGACT CCTACGGGAG GCAGCAGTGG 420 GGAATATTGC ACAATGGGCG CAAGCCTGAT GCAGCCATGC CGCGTGTATG AAGAAGGCCT 480 TCGGGTTGTA AAGTACTTTC AGCGGGGAGG AAGGGAGTAA AGTTAATACC TTTGCTCATT GACGTTACCC GCAGAAGAAG CACCGGCTAA CTCCGTGCCA GCAGCCGCGG TAATACGGAG 540 GGTGCAAGCG TTAATCGGAA TTACTGGGCG TAAAGCGCAC GCAGGCGGTT TGTTAAGTCA 600 GATGTGAAAT CCCCGGGCTC AACCTGGGAA CTGCATCTGA TACTGGCAAG CTTGAGTCTC 660 GTAGAGGGGG GTAGAATTCC AGGTGTAGCG GTGAAATGCG TAGAGATCTG GAGGAATACC 720 GGTGGCGAAG GCGGCCCCCT GGACGAAGAC TGACGCTCAG GTGCGAAAGC GTGGGGAGCA 780 AACAGGATTA GATACCCTGG TAGTCCACGC CGTAAACGAT GTCGACTTGG AGGTTGTGCC 840 CTTGAGGCGT GGCTTCCGGA GCTAACGCGT TAAGTCGACC GCCTGGGGAG TACGGCCGCA 900 AGGTTAAAAC TCAAATGAAT TGACGGGGGC CCGCACAAGC GGTGGAGCAT GTGGTTTAAT 960 TCGATGCAAC GCGAAGAACC TTACCTGGTC TTGACATCCA CGGAAGTTTT CAGAGATGAG 1020 AATGTGCCTT CGGGAACCGT GAGACAGGTG CTGCATGGCT GTCGTCAGCT CGTGTTGTGA 1080



AATGTTGGGT	TAAGTCCCGC	AACGAGCGCA	ACCCTTATCC	TTTGTTGCCA	GCGGTCCGGC	1140
CGGGAACTCA	AAGGAGACTG	CCAGTGATAA	ACTGGAGGAA	GGTGGGGATG	ACGTCAAGTC	1200
ATCATGGCCC	TTACGACCAG	GGCTACACAC	GTGCTACAAT	GGCGCATACA	AAGAGAAGCG	1260
ACCTCGCGAG	AGCAAGCGGA	CCTCATAAAG	TGCGTCGTAG	TCCGGATTGG	AGTCTGCAAC	1320
TCGACTCCAT	GAAGTCGGAA	TCGCTAGTAA	TCGTGGATCA	GAATGCCACG	GTGAATACGT	1380
TCCCGGGCCT	TGTACACACC	GCCCGTCACA	CCATGGGAGT	GGGTTGCAAA	AGAAGTAGGT	1440
AGCTTAACCT	TCGGGAGGGC	GCTTACCACT	TTGTGATTCA	TGACTGGGGT	GAAGTCGTAA	1500
CAAGGTAACC	GTAGGGGAAC	CTGCGGTTGG	ATCACCTCCT	TA		1542

(2) INFORMATION FOR SEQ ID NO:159:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1513 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:159:

60	TAATACATGC	GCGGCGTGCC	GTGAACGCTG	CTGGCTCAGA	GAGTTTGATC	TTTTTATGGA
120	GGGTGAGTAA	AGTGGCGCAC	GAAGTGGATT	TAGCTTGCTA	ATGAAGCTTC	AAGTCGAACG
180	TAATACTCTA	AAACGACTGC	CAACAGTTGG	CACAAGAGGA	ATCTGCCCTA	GGTATAGTTA
240	AGACTATATA	GTGTAGGATG	AAGTTTTTCG	TGAGTAGGGA	TAACACAAGT	TACTCCTGCT
300	TGGTCTGAGA	GACGCTTAAC	CCAAGGCTAT	TAATGGCTTA	GTTGGTAAGG	GTATCAGCTA
360	GCAGCAGTAG	CCTACGGGAG	GGTCCAGACT	ACTGAGACAC	TCACACTGGA	GGATGATCAG
420	ATGACACTTT	CGCGTGGAGG	GCAGCAACGC	AAACCCTGAC	GCAATGGGGG	GGAATATTGC
480	AATAAGCACC	GTACCTAAGG	AATTCTGACG	CTTAGGGAAG	AACTCCTTTT	TCGGAGCGTA
540	TCGGAATCAC	CAAGCGTTAC	ACGGAGGGTG	CCGCGGTAAT	GTGCCAGCAG	GGCTAACTCC
600	TGGCTTAACC	TGAAATCTAA	AAGTCTCTTG	GCGGATTATC	GGGCGCGTAG	TGGGCGTAAA
660	AATTGGTGGT	AGGCAGATGG	AGTGAGGGAG	GATAGTCTAG	TTGGGAAACT	ATTAAACTGC
720	TCTGCTGGAA	GCGAAGGCGA	AATACCCATT	TATCACCAAG	AATCCGTAGA	GTAGGGGTAA
780	CCCTGGTAGT	GGATTAGATA	GGAGCAAACA	GAAAGCGTGG	GCTAAGGCGC	CTCAACTGAC
840	AATGCAGCTA	TCATCTCAGT	GGGGTGCTAG	ACTAGTTGTT	AACGATGTAC	CCACGCCCTA
900	AGGAATAGAC	TAAAACTCAA	GTCGCAAGAT	GGGGAGTACG	TGTACCGCCT	ACGCATTAAG
960	AGAACCTTAC	AGATACGCGA	TTTAATTCGA	GAGCATGTGG	ACAAGCGGTG	GGGGACCCGC
1020	CTAGAACTTA	TGCTAGCTTG	GATAAGAGGG	ACCTTTTAGA	TATCCTAAGA	CTGGGCTTGA

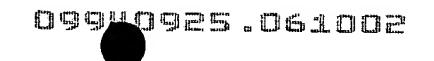
GAGACAGGTG	CTGCACGGCT	GTCGTCAGCT	CGTGTCGTGA	GATGTTGGGT	TAAGTCCCGC	1080
AACGAGCGCA	ACCCACGTAT	TTAGTTGCTA	ACGGTTCGGC	CGAGCACTCT	AAATAGACTG	1140
CCTTCGTAAG	GAGGAGGAAG	GTGTGGACGA	CGTCAAGTCA	TCATGGCCCT	TATGCCCAGG	1200
GCGACACACG	TGCTACAATG	GCATATAGAA	TGAGACGCAA	TACCGCGAGG	TGGAGCAAAT	1260
СТАТААААТА	TGTCCCAGTT	CGGATTGTTC	TCTGCAACTC	GAGAGCATGA	AGCCGGAATC	1320
GCTAGTAATC	GTAGATCAGC	CATGCTACGG	TGAATACGTT	CCCGGGTCTT	GTACTCACCG	1380
CCCGTCACAC	CATGGGAGTT	GATTTCACTC	GAAGCCGGAA	TACTAAACTA	GTTACCGTCC	1440
ACAGTGGAAT	CAGCGACTGG	GGTGAAGTCG	TAACAAGGTA	ACCGTAGGAG	AACCTGCGGT	1500
TGGATCACCT	CCT					1513

(2) INFORMATION FOR SEQ ID NO:160:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1555 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double

 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:160:

TTTTATGGAG	AGTTTGATCC	TGGCTCAGGA	TGAACGCTGG	CGGCGTGCCT	AATACATGCA	60
AGTCGAGCGA	ACGGACGAGA	AGCTTGCTTC	TCTGATGTTA	GCGGCGGACG	GGTGAGTAAC	120
ACGTGGATAA	CCTACCTATA	AGACTGGGAT	AACTTCGGGA	AACCGGAGCT	AATACCGGAT	180
AATATTTTGA	ACCGCATGGT	TCAAAAGTGA	AAGACGGTCT	TGCTGTCACT	TATAGATGGA	240
TCCGCGCTGC	ATTAGCTAGT	TGGTAAGGTA	ACGGCTTACC	AAGGCAACGA	TACGTAGCCG	300
ACCTGAGAGG	GTGATCGGCC	ACACTGGAAC	TGAGACACGG	TCCAGACTCC	TACGGGAGGC	360
AGCAGTAGGG	AATCTTCCGC	AATGGGCGAA	AGCCTGACGG	AGCAACGCCG	CGTGAGTGAT	420
GAAGGTCTTC	GGATCGTAAA	ACTCTGTTAT	TAGGGAAGAA	CATATGTGTA	AGTAACTGTG	480
CACATCTTGA	CGGTACCTAA	TCAGAAAGCC	ACGGCTAACT	ACGTGCCAGC	AGCCGCGGTA	540
ATACGTAGGT	GGCAAGCGTT	ATCCGGAATT	ATTGGGCGTA	AAGCGCGCGT	AGGCGGTTTT	600
TTAAGTCTGA	TGTGAAAGCC	CACGGCTCAA	CCGTGGAGGG	TCATTGGAAA	CTGGAAAACT	660
TGAGTGCAGA	AGAGGAAAGT	GGAATTCCAT	GTGTAGCGGT	GAAATGCGCA	GAGATATGGA	720
GGAACACCAG	TGGCGAAGGC	GACTTTCTGG	TCTGTAACTG	ACGCTGATGT	GCGAAAGCGT	780
GGGGATCAAA	CAGGATTAGA	TACCCTGGTA	GTCCACGCCG	TAAACGATGA	GTGCTAAGTG	840
TTAGGGGGTT	TCCGCCCCTT	AGTGCTGCAG	CTAACGCATT	AAGCACTCCG	CCTGGGGAGT	900
ACGACCGCAA	GGTTGAAACT	CAAAGGAATT	GACGGGGACC	CGCACAAGCG	GTGGAGCATG	960



TGGTTTAATT CGAAGCAACG CGAAGAACCT TACCAAATCT TGACATCCTT TGACAACTCT	1020
AGAGATAGAG CCTTCCCCTT CGGGGGACAA AGTGACAGGT GGTGCATGGT TGTCGTCAGC	1080
TCGTGTCGTG AGATGTTGGG TTAAGTCCCG CAACGAGCGC AACCCTTAAG CTTAGTTGCC	1140
ATCATTAAGT TGGGCACTCT AAGTTGACTG CCGGTGACAA ACCGGAGGAA GGTGGGGATG	1200
ACGTCAAATC ATCATGCCCC TTATGATTTG GGCTACACAC GTGCTACAAT GGACAATACA	1260
AAGGGCAGCG AAACCGCGAG GTCAAGCAAA TCCCATAAAG TTGTTCTCAG TTCGGATTGT	1320
AGTCTGCAAC TCGACTACAT GAAGCTGGAA TCGCTAGTAA TCGTAGATCA GCATGCTACG	1380
GTGAATACGT TCCCGGGTAT TGTACACACC GCCCGTCACA CCACGAGAGT TTGTAACACC	1440
CGAAGCCGGT GGAGTAACCT TTTAGGAGCT AGCCGTCGAA GGTGGGACAA ATGATTGGGG	1500
TGAAGTCGTA ACAAGGTAGC CGTATCGGAA GGTGCGGCTG GATCACCTCC TTTCT	1555
(2) INFORMATION FOR SEQ ID NO:161:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 46 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
(ii) MOLECULE TYPE: RNA (genomic)	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:161:	
GAAUACUCAA GCUUGCAUGC CUGCAGGUCG ACUCUAGAGG AUCCCC	46
(2) INFORMATION FOR SEQ ID NO:162:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 141 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
(ii) MOLECULE TYPE: DNA (genomic)	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:162:	
TTGACAATTA ATCATCGGCT CGTATAATGT GTGGAATTGT GAGCGGATAA CAATTTCACA	60
CAGGAAACAG CGATGAATTC GAGCTCGGTA CCCGGGGATC CTCTAGAGTC GACCTGCAGG	120
CATGCAAGCT TGGCACTGGC C	141
(2) INFORMATION FOR SEQ ID NO:163:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 144 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:163:			
AGATCTCGAT CCCGCGAAAT TAATACGACT CACTATAGGG AGACCACAAC GGTTTCCCTC	60		
TAGAAATAAT TTTGTTTAAC TTTAAGAAGG AGATATACAT ATGGCTAGCA TGACTGGTGG	120		
ACAGCAAATG GGTCGGATCC GGCT			
(2) INFORMATION FOR SEQ ID NO:164:			
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 71 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 			
(ii) MOLECULE TYPE: DNA (genomic)			
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:164:			
TAATACGACT CACTATAGGG AGACCGGAAT TCGAATTCCG TGTATTCTAT AGTGTCACCT	60		
AAATCGAATT C	71		
(2) INFORMATION FOR SEQ ID NO:165:			
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 228 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 			
(ii) MOLECULE TYPE: DNA (genomic)			
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:165:			
CGCCAGGGTT TTCCCAGTCA CGACGTTGTA AAACGACGGC CAGTGAATTG TAATACGACT	60		
CACTATAGGG CGAATTCGAG CTCGGTACCC GGGGATCCTC TAGAGTCGAC CTGCAGGCAT	120		
GCAAGCTTGA GTATTCTATA GTGTCACCTA AATAGCTTGG CGTAATCATG GTCATAGCTG	180		
TTTCCTGTGT GAAATTGTTA TCCGCTCACA ATTCCACACA ACATACGA	228		